5.1.6	Compugen Ltd.
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March 30, 2005, 21:09:54 ; Search time 225.955 Seconds (without alignments) 349.180 Million cell updates/sec Run on:

US-10-828-343-2 1095

score: Perfect

1 MCWFKLWSLLLVGSLLVSGT.......GQAVRVLDSIPDVTPDVHDK 204 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* 1: geneserm1006-Database

geneseqp1980s:*
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geneseqp2001s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

lon	Human her	Human her	Kaposi sa	Kaposi's	Interleuk	Interleuk	Human mod	Interleuk	Human int	Interleuk	Human mod	Polypepti	Human int	Human IL-	Human fus	Human fus	Human IL-	Human mod	Human mod	Human mod					
Description	Aaw40103	Aaw23944	Aaw74570	Aaw95015	Aaw02611	Aaw02610	Ad189593	Aaw08477	Abp72702	Aaw08476	Ad189567	Aap81162	Aau99248	Aau99249	Aau99250	Aau99601	Aaw07200	Aaw58519	Aaw92803	Aaw36847	Aaw36846	Aar77387	Ad189594	Ad189586	Ad189584
DI	AAW40103	AAW23944	AAW74570	AAW95015	AAW02611	AAW02610	ADL89593	AAW08477	ABP72702	AAW08476	ADL89567	AAP81162	AAU99248	AAU99249	AAU99250	AAU99601	AAW07200	AAW58519	AAW92803	AAW36847	AAW36846	AAR77387	ADL89594	ADL89586	ADL89584
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% Query Match	100.0	100.0	100.0	90.6	17.2	17.1	17.0	16.9	16.9	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.7	16.7	16.7	16.7
Score	1095	1095	1095	992	188	187	186	185.5	185.5	184.5	184	184	184	184	184	184	183.5	183.5	183.5	183.5	183.5	183	183	183	183
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ALIGNMENTS

Human herpesvirus 8 (HHV-8) interleukin-6. AAW40103 standard; protein; 204 AA (revised)
(first entry) 27-AUG-2003 15-JUL-1998 AAW40103; AAW40103

DL-B; thymidylate synthase; dihydrofolate reductase; primer; HHV-8; Bcl-2 homologue; IE-1A; IE-1B; viral macrophage inhibitory protein; Kaposi's sarcoma; beta-chemokine-like; amplification; PCR; vIL-6.

Human herpesvirus 8.

WO9804284-A1.

05-FEB-1998.

97WO-US012931. 24-JUL-1997;

96US-0022591P. 25-JUL-1996;

(UYJO) UNIV JOHNS HOPKINS.

Hardwick JM; Nicholas J, Reitz MR, Hayward GS,

WPI; 1998-130422/12.

New human herpes virus gene region containing 8 open reading frames -useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based large cell lymphoma.

Claim 1, Page 59-60; 84pp; English.

The sequence represents a novel human herpesvirus 8 (HHV-8) interleukin-6. The invention claims for novel genes, which includes the viral interleukin-6 gene, found at the divergent DL-B locus. HHV-8 divergent locus DL-B lies between open reading frames 11 and 17. Sequencing of the HHV-8 divergent locus DL-B revealed the presence of nine viral ORFs with gene products related to cellular proteins. These proteins include the thymidylate synthase (TS, AAM40100), dihydrofolate reductase (DHFR, see AAM40101), Bcl-2 homologue (AAM40102), IE-1A (AAM40107), IE-1B (AAM40108) macrophage inhibitory protein (MMIP)-1A (AAM40104) and -1B (AAM40105) and beta-chemokine-like (BCK, AAM40106) protein. The invention claims the

infections and diseases as mentioned above

Sequence 204 AA;

SXS

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mentioned proteins and a polynucleotide containing HHV-8 genes encoding one or more of these proteins. The invention also claims that the polynucleotide and the proteins may be used directly or indirectly, e.g. using antibodies to the proteins, to diagnose an HHV-8 associated disease, e.g. Kaposi's sarcoma, Castleman's disease, multiple myeloma and body cavity based large cell lymphoma (BCBL). The proteins have also been claimed to be useful in screening compounds for drugs to treat HHV-8 diseases. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                                                                                                                                                                                               NVDVMELLIKTIGWDIQEELNKITKTHYSPPKFDRGLIGRLQGLKYWVRHFASFYVLSAM 180
                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viral interleukin-6 produced recombinantly from human herpes virus 8 DNA - and related nucleic acid and antibodies, used for diagnosis and treatment of herpes 8 infection or related diseases, e.g. Kaposi sarcoma.
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                                                                                                                                                                                                                                             1 MCWFKLMSLLLVGSLLVSGTRGKLPDAPEFEKDLLIQRLNWMLWVIDECFRDLCYRTGIC
                                                                                                                                                                                                                                                                                                    KGILEPAAI FHLKLPAINDTDHCGLIGFNETSCLKKLADGFPEFEVLFKFLTTEFGKSVI
                                                                                                                                                                                                                                                                                     KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVI
                                                                                                                                                                                                                                                                                                                                              NVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAM
                                                                                                                                                                                                                            1 MCWFKLWSLLLVGSLLVSGTRGKLPDAPEFEKDLLIQRLNWMLWVIDECFRDLCYRTGIC
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interleukin-6; IL-6; human herpesvirus 8; HHV8; shotgun-cloning;
                                                                                                                                                                                               °,
                                                                                                                                                                 Length 204;
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                                                                                                                                                                                               0; Indels
                                                                                                                                                                 100.0%; Score 1095; DB 2; 100.0%; Pred. No. 1.2e-117;
                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          EKFAGQAVRVLDSIPDVTPDVHDK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW23944 standard; protein; 204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human herpesvirus 8 interleukin-6.
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                                                                                                                                                                                               Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-120781/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human herpesvirus 8
                                                                                                                                                                               Local Similarity
                                                                                                                                      Sequence 204 AA;
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The interleukin-6 (IL-6) and protein AAW21945 derived from the sequence can be used to detect antibodies and antibodies can be used to detect IL-6. This can be used for the diagnosis of HRV8 infection or associated diseases such as Kaposi sarcoma or kidney cell carcinoma. Antibodies, proteins and the gene sequence can all be used in the treatment of

Claim 2; Fig 2; 19pp; English.

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                                                                                                                          61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVI 120
                                                                                                                                                                                                       NVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virus/interleukin-6, used in the method of the invention. In this method, an antiviral agent effective against Kaposi sarcoma herpes-like virus (KSNV), is used to prevent progression of MGUS to multiple myeloma or related malignancy. KHSV- and/or interleukin-6 related disorders such as specifically Alzheimer's disease, multiple sclerosis, rheumatoid
                                                                               1 MCWFKLWSLLLVGSLLVSGTRGKLPDAPEFEKDLLIQRLNWMLWVIDECFRDLCYRTGIC 60
                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treatment of multiple myeloma and monoclonal myopathy with antiviral agent - active against Kaposi sarcoma virus, or with inhibitory nucleic acid or antibody against this virus.
                                                                                                                                            61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVI
                                                              1 MCWFKLWSLLLVGSLLVSGTRGKLPDAPEFEKDLLIQRLNWMLWVIDECFRDLCYRTGIC
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaposi sarcoma herpes-like virus/interleukin-6; PCR; primer; antiviral agent; multiple myeloma; vaccine; rheumatoid arthritis; monoclonal gammopathy of undetermined significance; MGUS; malignant; interleukin-6; Alzheimer's disease; multiple sclerosis; scleroderma; systemic lupus erythematosus; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of the kaposi sarcoma herpes-like
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 Length 204;
                               Indela
, DB 2; 1
1.2e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaposi sarcoma herpes-like virus/interleukin-6.
                             0; Mismatches
100.0%; Score 1095; 100.0%; Pred. No. 1.3
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                                                                                                                                                                                                                                                                        Vescio RA;
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                                                                                                                                                                                                                                                                                                                                                                    AAW74570 standard; protein; 204 AA
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97US-00967504.
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                                 Conservative
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(RETT/) RETTIG M.B.
(VESC/) VESCIO R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-480765/41.
                Similarity
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                               204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newly isolated or recombinant polynucleotide encoding mammalian cytokine interleukin-B30 (IL-B30), including fragments - useful for regulating activation, development, differentiation and function of various cell types, and for diagnosing and treating conditions associated with IL-B30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to mammalian cytokine interleukin-B30 (IL-B30) polypeptides. Host cells containing a vector comprising the IL-B30 nucleic acids are used for the recombinant production of the proteins. The polynucleotides are useful for diagnosis of IL-B30 mediated conditions, and forensic science (e.g. to distinguish rodent from human, or as a marker to distinguish between different cells exhibiting differential expression or medification patterns). The IL-B30 (including fragments), together with antibodies that bind to IL-B30 are useful for teaching purposes. They are also used for treating conditions associated
arthritis, systemic lupus erythematosus, scleroderma and malignancies of kidney or head/neck. The vaccines (comprising a KHSV-specific immunogen) is used to produce a therapeutic and/or prophylactic response
                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation; inflammatory condition; drug screening; human; IL-6.
                                                                                                                       1 MCWFKLWSLLLVGSLLVSGTRGKLPDAPEFEKDLLIQRLNWMLWVIDECFRDLCYRTGIC
                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     Kaposi's sarcoma herpes virus interleukin-6 (IL-6) polypeptide.
                                                                 Length 204;
                                                                                       0; Indels
                                                                 100.0%; Score 1095; DB 2;
100.0%; Pred. No. 1.2e-117;
                                                                                       0; Mismatches
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(first entry)
                                                                                      Matches 204; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human herpesvirus 8
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                                                                             Similarity
                                           Sequence 204 AA;
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21-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist; bovine; granulocyte colony stimulating factor; bG-CSF; receptor; gp130; thrombocytopaenia; haematopoietic progenitor cell; rheumatoid arthritis; bone marrow transplantation; gene therapy; multiple myeloma; leukaemia; breast cancer; infectious disease; bone marrow progenitor cell; therapy;
with abnormal physiology or development, including inflammatory conditions. The polypeptide cytokine should mediate cytokine synthesis and proliferation in cells. IL-B30 is useful for drug screening to identify compounds having binding affinity to IL-B30. The present sequence represents a Kaposis's sarcoma herpes virus IL-6. (Updated on -AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                       1 TRGKLPDAPEFEKDLLIQRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVLDSIPDVTP
                                                                                                                                                                                                                                                                                                            20 TRGKLPDAPEFEKDLLIQRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND
                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                    Length 185;
                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                             90.6%; Score 992; DB 2; Le
100.0%; Pred. No. 8.2e-106;
tive 0; Mismatches 0;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVHDK 185
                                                                                                                                                                   Sequence 185 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                            185;
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24-FEB-1997
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Location/Qualifiers

'note= "Q75Y"

Misc-difference Misc-difference Misc-difference /note= "Q183A"

WO9618648-A1

/note= 'note=

Misc-difference 176 Misc-difference 183

/note=

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AAW02610-W02612 represent human interleukin-6 (IL-6) mutants (see
AAW02609 for wild type sequence), with an increased specificity for the
specific receptor. These sequences were identified using the method of
the invention. The method comprises comparing IL-6 with the sequence of
the bovine granulocyte colony stimulating factor (bG-CSF). On the basis
of this comparison a 3-dimensional model of IL-6 is formulated, which
allows the identification of residues that form the site of interaction
with the specific receptor, and those that constitute the site of
interaction with gpl30. The method can be used to identify superagonists,
antagonists, and superantagonists of IL-6. The IL-6 superagonists
identified by this method can be used for the treatment of
thrombocytopaenia, and for the ex vivo expansion of human haematopoietic
progenitor cells for bone marrow transplantation and gene therapy. They
can also be used for the treatment of breast cancer, leukaemia, and
progenitor cells. The antagonists and superantagonists identified by the
method (see AAW03476-W08476) can be used for the treatment of cidseases
method see AAW03476-W08476) can be used for the treatment of idiseases
                                                                                                                                Identifying interleukin-6 super-agonists and (super)antagonists - using a 3-dimensional model of bovine granulocyte colony stimulating factor to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       characterised by the overproduction of IL-6, particularly multiple myeloma, rheumatoid arthritis, postmenopausal osteoporosis, and systemic lupus erythematosus. The method can also be used to identify IL-6 variants with a greater affinity for the specific receptor, or variants with a reduced or abolished affinity for gpl30. (Updated on 25-MAR-2003
                           Toniatti C;
                           Lahm A,
                                                                                                                                                                                                                                             Claim 8; Page ?; 26pp; English.
                           Savino R,
                                                                                                                                                                                        identify binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with a reduced or abo
to correct PR field.)
                         Ciliberto G,
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Sequence 184 AA;

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88 FNETSCLKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTH 147
                                                                                                                                                            87
                                                                                                      77
                                                                                         18 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCYFIG
                                                                     28 PEFEKDLLIQRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIG
                                    ;
0
17.2%; Score 188; DB 2; Length 184; 26.2%; Pred. No. 5.8e-13; Live 38; Mismatches 83; Indels
                                                                                                                                                                                                            148 YSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVL 191
                                                                                                                                                                                                                                 138 TPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEFLIRSLRAL 181
                                    43; Conservative
                    Local Similarity
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                                    Matches
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AAW02610 standard; protein; 184 AA (first entry) (revised) 25-MAR-2003 24-FEB-1997 AAW02610; AAW02610

11D AAW0

XX AC AAW0

XX DT 25-M

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Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist; bovine; granulocyte colony stimulating factor; bG-CSF; receptor; gpl30; thrombocytopaenia; haematopoietic progenitor cell; rheumatoid arthritis; bone marrow transplantation; gene therapy; multiple myeloma; leukaemia; breast cancer; infectious disease; bone marrow progenitor cell; therapy; postmenopausal osteoporosis; systemic lupus erythematosus; hormone. Interleukin-6 (Q75Y, S76I, Q175I, S176R, Q183A).

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AM02609 for wild type sequence), with an increased specificity for the specific receptor. These sequences were identified using the method of the bovine granulocyte colony simulating factor (bd-CSF). On the basis of this comparison a 3-dimensional model of IL-6 is formulated, which allows the identification of residues that form the site of interaction with the specific receptor, and those that constitute the site of interaction with appl30. The method can be used to identify superantagonists of interaction with applantagonists of interaction with a method can be used for the treatment of thrombocytopaenia, and for the expansion of human haematopoietic thrombocytopaenia, and for the treatment of bused for the treatment of bused for the treatment of breast cancer, leukemia, and infectious diseases or diseases connected with disorders of bone marrow progenitor cells for bone marrow transplantation and gene therapy. They can also be used for the treatment of bone marrow progenitor cells. The antagonists and superantagonists of bone marrow progenitor cells. The antagonists and superantagonists identified by the overproduction of IL-6, particularly multiple myeloma, rheumatoid arthritis, postmenopausal osteoporosis, and systemic lupus expthematosus. The method can also be used to identify IL-6 variants with a reduced or abolished affinity for the specific receptor, or variants with a reduced or abolished affinity for the specific receptor, or variants with a reduced or abolished affinity for the specific receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 FNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAIT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying interleukin-6 super-agonists and (super)antagonists - using 3-dimensional model of bovine granulocyte colony stimulating factor to identify binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 PEFEKDLLIQRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW02610-W02612 represent human interleukin-6 (IL-6) mutants (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 YSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.1%; Score 187; DB 2; 26.2%; Pred. No. 7.5e-13; tive 38; Mismatches 83.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciliberto G, Savino R, Lahm A, Toniatti C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page ?; 26pp; English.
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Les 43; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New modified cytokines with increased resistance to proteolysis, useful for diagnosing and treating diseases such as infections, allergies, heart diseases, cancer, liver disorders, autoimmune diseases or diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                               cytokine; proteolysis; interferon; IFN; interleukin-10; IL-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             long-chain cytokine family; short-chain cytokine family; infection; allergy; heart disease; cancer; liver disorder; autoimmune disease; growth disorder; diabetes; neurodegenerative disease; antimicrobial; antiallergic; cytostatic; immunosuppressive; antidiabetic; neuroprotective; mutant; mutein.
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138 TPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEFLIRSLRAL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84; Indels
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; Pred. No. 9.7e-13;
37; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drittanti L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 927; 316pp; English
                                                                                                                                                                                                                                                                                                                                                              Human modified cytokine protein #875.
                                                                                                                                                            ADL89593 standard; protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vega M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-SEP-2003; 2003WO-IB004347.
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21-MAR-2003; 2003US-0457135P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                             ADL89593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
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Identifying interleukin-6 super-agonists and (super)antagonists - using a 3-dimensional model of bovine granulocyte colony stimulating factor to
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                                                                                                                                                                                                            Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist; bovine; granulocyte colony stimulating factor; DG-CSF; receptor; gpj30; thrombocytopaenia, haematopoietic progenitor cell; rheumatoid arthritis; bone marrow transplantation; gene therapy; multiple myeloma; leukaemia; breast cancer; infectious disease; bone marrow progenitor cell; therapy; postmenopausal osteoporosis; systemic lupus erythematosus; hormone.
                148 YSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toniatti C;
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                         AAW08477 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lahm A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page ?; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "V121D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Q175I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Q183A"
                                                                                                                                                                                                                                                                                                                                                              'note= "Y31D"
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Q75Y"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "S761"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94IT-RM000805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-IT000216
                                                                                                                                                             (first entry)
                                                                                                                                                                                    Interleukin-6 variant #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ciliberto G, Savino R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identify binding sites.
                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note=
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                                                                                                                                               (revised)
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                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-DEC-1994;
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                                                                                                                                             25-MAR-2003
24-FEB-1997
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                                                                                                                   AAW08477;
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model of IL-6 is formulated, which allows the identification of residues
that form the site of interaction with the specific receptor, and those
that constitute the site of interaction with applion The method can be
used to identify superagonists, antagonists, and superantagonists of IL-
treatment of thrombocytopaenia, and for the ex vivo expansion of human
hematopoletic progenitor cells for bone marrow transplantation and gene
therapy. They can also be used for the treatment of breast cancer,
cleukaemia, and infectious diseases or diseases connected with disorders
of bone marrow progenitor cells. The antagonists and superantagonists
of bone marrow progenitor cells. The antagonists and superantagonists
cleukaemia, and infectious diseases or diseases connected with disorders
of bone marrow progenitor cells. The antagonists and superantagonists
cleukaemia rheumatoid arthritis, postmenopausal osteoporosis, and systemic
lupus erythematosus. The method can also be used to identify IL-6
variants with a greater affinity for the specific receptor (see AAW02610-
W02612), or variants with a reduced or abolished affinity for gpl30.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 KKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFD 154
                                                                                                                                                                                                                                                                                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                             --- CYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCL
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; interleukin-6; receptor; DS-sIL-6R; antibacterial; virucide;
anti-HIV; antirheumatic; antiarthritic; antiinflammatory;
immunosuppressive; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human interleukin-6-receptor isoform DS-sIL-6R fusion protein.
                                                                                                                                                                                                                                                                                                                                     16.9%; Score 185.5; DB 2; Length 184; 28.0%; Pred. No. 1.1e-12; ive 31; Mismatches 71; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 RGLLGRLOGLKYWVRHFASFYVLSAMEKFAGQAVRVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP72702 standard; protein; 570 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .. .364
'label= DS-sIL-6R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      561. .570
/label= C-myc tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365. .376
/label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377. .560
/label= IL-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-AUG-2002; 2002WO-GB003581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2001; 2001GB-00019015
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                                                                                                                                                                                                                                                                                                                                                                        44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       46 IDECFRDL--
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                        Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003014359-A2
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Synthetic.
Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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The present sequence is the protein sequence of a novel fusion protein comprising a soluble form of the human interleukin-6 receptor, denoted DS -81L-6K (see also ABP72709), joined via a peptide linker to a human IL-6 molecule (see also ABP72709), with a C-terminal c-myc tag sequence. Administration of this fusion protein results in the increased expression of one or more of MIP-lalpha, MIP-lbeta and RAWYES complete with HIV for binding to CCR5 and effectively suppress HIV entry. The fusion protein can be used in the treatment of any disease in which the infectious agent binds to CCR5, especially M-trophic strains of HIV. The invention also provides a nucleic acid molecule encoding the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein in the host cell. The fusion protein, nucleic acid or vector can be used in the manufacture of a medicament for the prophylaxis or treatment of an infectious disease (especially AIDS caused by a M-trophic strain of HIV, or bacterial peritonitis), an inflammatory disorder or an immunological disorder (especially rheumatoid arthitis), when it is desirable to increase or resolve an immune response (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                429 SKEALAENNINIDEMAEKDGCFQSGFNEETCLVKIITGILEFEVVLEYLQNRFESSEEQA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 ILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVINV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 DVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAMEK 182
                                                                                                                                                      New fusion protein having a functional IL-6 and DS-sIL-6R molecule, useful for the manufacture of a medicament for the prophylaxis or treatment of an infectious disease, and an inflammatory or immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist; bovine; granulocyte colony stimulating factor; bG-CSF; receptor; gpl30; thrombocytopaenia; hamatopoietic progenitor cell; rheumatoid arthritis; bone marrow transplantation; gene from poietic progen; multiple myeloma; leukaemia; breast cancer; infectious disease; bone marrow progenitor cell; therapy; postmenopausal osteoporosis; systemic lupus erythematosus; hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 SGGGGSLEPVPPGEDSKDVAAPHRQPLTSSERTDKQIRYILDGISALRKETCNKSNMCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 SGTRGKLPDAP--EFEKDLLI------QRLNWMLWVIDECFRDLCYRTGICKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.9%; Score 185.5; DB 6; Length 570; 25.9%; Pred. No. 5e-12; ive 36; Mismatches 89; Indels 15,
(UYCA-) UNIV COLLEGE CARDIFF.
(UYWA-) UNIV WALES COLLEGE OF MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW08476 standard; protein; 184 AA.
                                                                                                                                                                                                                                                                   Disclosure, Fig 5; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.99
Watches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin-6 variant #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        549 FLQSSLRAL 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                    Topley N;
                                                                                                               WPI; 2003-256588/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 570 AA;
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                                                                    Jones SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW08476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
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    8
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KKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFD 154

155 RGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVL 191

84 94

-----CYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCL

46 IDECFRDL-

95

원 ð 요 ò

25 IDKOIRDILDFISALRKETCNKSNMCESSKEALAENNINLPKMAEKDGCFYIGFNEETCL

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AW02609 for wild type sequence), with greater affinity for the receptor, which can be used as IL-6 antagonists and superantagonists. These sequences were identified using the method of the invention. The method comprises comparing IL-6 with the bovine granulocyte colony stimulating factor (bG-CSF) sequence. On the basis of this comparison a 3-dimensional model of IL-6 is formulated, which allows the identification of residues that form the site of interaction with the specific receptor, and those that constitute the site of interaction with gpl30. The method can be used to identify superagonists, antagonists, and superantagonists of IL-6 of Thrombocytopaenia, and for the ex vivo expansion of human hemmatopoietic progenitor cells for bone marrow transplantation and gene therapy. They can also be used for the treatment of breast cancer. Clenkaemia, and infectious diseases onnected with disorders of bone marrow progenitor cells for bone marrow transplantation and gene therapy. They can also be used for the treatment of breast cancer. Clenkaemia, and infectious diseases onnected with disorders of bone marrow progenitor cells. The antagonists and superantagonists clenkaemia cancer the method can be used for the treatment of diseases.

Characterised by the method can be used for the treatment of diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lupus erythematosus. The method can also be used to identify IL-6 variants with a greater affinity for the specific receptor (see AAW02610-W02612), or variants with a reduced or abolished affinity for gpl30. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       characterised by the overproduction of IL-6, particularly multiple myeloma, rheumatoid arthritis, postmenopausal osteoporosis, and systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying interleukin-6 super-agonists and (super)antagonists - using 3-dimensional model of bovine granulocyte colony stimulating factor to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW08476-W08478 represent human interleukin-6 (IL-6) mutants (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toniatti C;
                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Savino R, Lahm A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page ?; 26pp; English.
                                                                                                                                                                                                                                                                                                                                 'note= "Q175I"
                                                                                                                                                                                                                                                      note= "S118R'
                                                                                                                                                                                                                                                                                          'note= "V121D"
                                                                                                                                                                                                                                                                                                                                                                     'note= "S176R'
                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Q183A
                                                                                                                                                                          note= "Q75Y"
                                                                                                                                                                                                                  note= "S761"
                                                                                              'note= "Y31D"
                                                                                                                                    'note= "G35F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-IT000216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identify binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-300575/30.
                                                                                                                                                                                                                                                                                                                                                   Misc-difference 176
                                                                                                                                                                                                                                                                        Misc-difference 121
                                                                                                                Misc-difference 35
                                                                                                                                                      Misc-difference
                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                Misc-difference
                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ciliberto G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-DEC-1994;
                      Homo sapiens
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resistance to proteolysis compared to unmodified cytokines. The invention also relates to nucleic acid molecules encoding the cytokines, a pharmaceutical composition comprising a nucleic acid molecule in a pharmaceutical carrier, and a method of generating a protein or peptide molecule having a predetermined property or activity, or a pre-selected altered phenotype. The modified cytokine is selected from a member of the long-chain cytokine family in a member of the family. The composition and method are useful for diagnosing and treating diseases such as infections, allergies, heart diseases, cancer, liver disorders, autoimmune diseases, growth disorders, diabetes or neurodegenerative diseases. This sequence represents a human modified cytokine protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified cytokines with increased resistance to proteolysis, useful for diagnosing and treating diseases such as infections, allergies, heart diseases, cancer, liver disorders, autoimmune diseases or diabetes.
                                                                                                                                                                                                                                          Human, cytokine; proteolysis; interferon; IFN; interleukin-10; IL-10; long-chain cytokine family; short-chain cytokine family; infection; allergy; heart disease; cancer; liver disorder; autoimmune disease; growth disorder; diabetes; neurodegenerative disease; antimicrobial; antiallergic; cytostatic; immunosuppressive; antidiabetic; neuroprotective; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to modified cytokines that exhibit increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 184; DB 8; Length 183; Pred. No. 1.7e-12;
Drittanti L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 901; 316pp; English.
                                                                                                                                                                                                             Human modified cytokine protein #849.
                                                                                                        Ź
                                                                                                      ADL89567 standard; protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vega M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.8%;
26.2%;
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                                                                                                                                                                            03-JUN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guyon T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-248447/23.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004022593-A2
                                                                                                                                                                                                                                                                                                                                                                       sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                     RESULT 11
                                                                                       ADL89567
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Gaps

11;

16.8%; Score 184.5; DB 2; Length 184; 28.0%; Pred. No. 1.5e-12; ive 31; Mismatches 71; Indels 11;

Query Match 16.8 Best Local Similarity 28.0 Matches 44; Conservative

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                                                            17 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLFKIAEKDGCFQSG 76
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   85; Indels
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 Mismatches
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86JP-00302699.
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18-DEC-1986;
13-MAY-1987;
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15-OCT-1990
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The invention relates to a polynucleotide comprising a first nucleotide sequence (NS1) comprising a LL6 (interleukin-6, an inflammatory cytokine) isogene selected from isogenes 1-11 and 13-18 given in the specification, where each isogene comprises the regions of NS1 and is further defined by the corresponding sequence of polymorphisms whose locations and identities are defined in the specification (PS2-PS6, PS8 and PS10-PS17), or a second nucleotide sequence (NS2) complementary to NS1.

Alternatively, the sequence comprises a coding sequence for an LL6 isogene. Also included are methods of haplotyping/ genotyping (and isogene. Also included are methods of haplotyping/ genotyping (and isogene) of the LL6 gene of an individual, identifying an association between a trait and at least one haplotype or haplotype pair of the LL6 gene, an isolated oligonucleotide for detecting a polymorphism in the LL6 gene, a recombinant non-human organism (III) transformed or transfected with the LL6 polymucleotide, an isolated fragment of the LL6 isogene comprising at least 10 and containing one of the indexified single- nucleotide polymorphism (SNP), an isolated the LL6 isogene comprising at least 10 and containing the latest and the Least one had the latest and the l
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                                                              | :: :| ::| | 173 QWLQDMTTHLILRSFKEFLQSSLRAL 198
166 YWVRHFASFYVLSAMEKFAGQAVRVL 191
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ker EA;
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Sausker E
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Parks KE,
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arthritis, Kaposi sarcoma (associated with human immunodeficiency virus infection, HIV), hypercalcaemia, bone disease, inflammatory disease, stunted growth and systemic onset, juvanile chronic arthritis. The methods are useful for improving the efficiency and reliability in the discovery and development of drugs and in the validation of IL6 as a drug target. The antibody is useful in diagnostic, prognostic and therapeutic methods and in expressing IL6 protein for use in screening for candidate drugs. The gene for IL6 is located on chromosome 7p21-p15. The present sequence is a interleukin-6 protein variant. Note: The present sequence is not shown in the specification but was created by the indexer using the IL6 sequence appearing as AAU99244 and the information on page 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.8%; Score 184; DB 5;
25.8%; Pred. No. 2e-12;
iive 38; Mismatches 92;
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196 RSFKEFLQSSLRAL 209
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recording to the control of control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 SVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVL 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The gene for IL6 is located on chromosome 7p21-p15. The present sequence is a interleukin-6 protein variant. Note: The present sequence is not shown in the specification but was created by the indexer using the IL6 sequence appearing as AAU99244 and the information on page 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 VGSLLVSGTRGKLPDAP-EFEKDL------LIQRLNWMLWVIDECFRDLCYRT 57
                                                                                                      Genetic variants of interleukin-6 isogenes for improving efficiency and reliability in drug development for treating myeloma, coronary artery disease, arthritis and Kaposi sarcoma.
                                                                                                                                                                                                                                                                            invention relates to a polynucleotide comprising a first nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 NACESSKEALAENNINLPRWAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFES
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  Sausker EA;
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                                                                                                                                                                                                                     Claim 29; Page; 86pp; English
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  Parks KE,
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  Nandabalan K,
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Human; interleukin-6; IL6; myeloma; arthritis; CAD; Kaposi sarcoma; coronary artery disease; inflammatory cytokine; hypercalcaemia; bone disease; inflammatory disease; HIV; human immunodeficiency virus infection; sunted growth; isogene; systemic onset juvenile chronic arthritis; haplotype; genotype; chromosome 7p21-p15; gene therapy; SNP; single nucleotide polymorphism.
                                                                                               Human interleukin-6, IL6, variant #6.
24-SEP-2002 (first entry)
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sapiens Ношо

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/note= "Wild-type Pro substituted by Ser"
                                                   'note= "Wild-type Pro substituted by Thr"
Key Location/Qualifiers
Misc-difference 31
                                                                           Misc-difference 3
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WO200238586-A2

09-NOV-2001; 2001WO-US047077. 16-MAY-2002

09-NOV-2000; 2000US-0247578P. 21-AUG-2001; 2001US-0313963P.

(GENA-) GENAISSANCE PHARM INC

Denton RR, Lachowicz M; Bentivegna SC, Bieglecki KM, Chew A, Nandabalan K, Parks KE, Sausker EA;

WPI; 2002-519290/55.

Genetic variants of interleukin-6 isogenes for improving efficiency and reliability in drug development for treating myeloma, coronary artery disease, arthritis and Kaposi sarcoma.

Claim 29; Page; 86pp; English.

The invention relates to a polynucleotide comprising a first nucleotide sequence (NS1) comprising a Li6 (interleukin-6, an inflammatory cytokine) isogene selected from isogenes 1-11 and 13-18 given in the specification, where each isogene comprises the regions of NS1 and is further defined by the corresponding sequence of polymorphisms whose locations and identities are defined in the specification (PS2-PS6, PS8 and PS10-PS17), as a second nucleotide sequence (NS2) complementary to NS1.

Alternatively, the sequence comprises a coding sequence for an IL6 isogene. Also included are methods of haplotyping/ genotyping (and isogene. Also included are methods of the IL6 gene of an individual, identifying an association between a trait and at least one haplotype or haplotype pair of the IL6 gene, a recombinant non-human organism (III) transformed or transfected with the IL6 polymucleotide, an isolated fragment of the IL6 isogene comprising at least 10 and containing one of the indentified single-nucleotide polymorphisms (SNP), an isolated the indentified single-nucleotide polymorphisms (SNP), an isolated polypeptide (or fragment) comprising an amino acid sequence which is a polypeptide (or fragment) comprising an amino acid sequence which is a polymorphic variant of IL6, an isolated monoclonal antibody specific for IL6, a computer system for storing and analysing polymorphism data for the IL6 gene, and a genome anthology for the IL6 gene. The IL6 care useful for treating myeloma, coronary artery disease (CAD), arthritis, Kaposi sarcoma (associated with human immunodeficiency virus infection, HIV), hypercalcaemia, bone disease, inflammatory disease, arthritis, The methods currentled growth and systemic onset juvenile chronic arthritis. The methods are useful for improving the efficiency and carlability in the discovery and development of drugs and in the validation of IL6 as a drug target. The antibody is useful in diagnostic, prognostic and therapeutic methods. The IL6 isogene is useful in studying the expression and function of IL6, and in expressing IL6 protein for use in screening for candidate drugs. The gene for IL6 is located on chromosome 7p21-p15. The present sequence

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                                                                                                                                                                                                                                                                                                                                          116 GKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFY 175
                                                                                                                                                                                                                                                                                                                                                                    134 ESSEEQARAVQMSTKVIlQFLQKKAKNIDAITTPDFTTNASLLTKLQAQNQWLQDMTTHL 193
                                                                                                                                                                                                               14 FSLGLLLVLPAAFPAPVTSGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCN 73
                                                                                                                                                                                        4 FKLWSLLLVGSL----LVSGTRGKLPDAPEFE----KDLLIQRLNWMLWVIDECFRDLCY 55
is a interleukin-6 protein variant. Note: The present sequence is not shown in the specification but was created by the indexer using the IL6 sequence appearing as AAU99244 and the information on page 29
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                                                                                                              Length 212;
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tive 42; Mismatches 96; Indels
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Job time: 227.955 secs
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194 ILRSFKEFLQSSLRAL 209
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Sequence 2, Appli
                                                                                                                                                                           March 30, 2005, 21:58:00; Search time 53.9731 Seconds (without alignments) 282.148 Million cell updates/sec
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1 MCWFKLWSLLLVGSLLVSGT.......GQAVRVLDSIPDVTPDVHDK 204
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-558-087-16

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US-08-54-74-16

US-08-945-529-12

US-07-918-181A-4

US-07-918-181A-8

US-07-918-181A-8

US-08-231-575-4

US-08-231-575-8

US-08-231-575-8

US-08-231-575-8

US-08-231-578-8

US-08-792-0198-9

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US-08-792-0198-9

US-08-792-0198-9

US-08-786-7

US-09-210-637-45

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     protein search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                                                 Run on:
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No.
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Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Patent No. 5186931 Sequence 1, Appli Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli		of Kaposi's Sarcoma rus 7 31 32 6	
2 US-09-008-482-2 1 US-08-609-973-1 1 US-08-567-047-2 US-08-567-048-2 6 5186931-1 1 US-07-632-070B-1 1 US-07-918-1181A-2 1 US-07-918-1181A-2 1 US-08-231-575-2 1 US-08-246-427A-5 2 US-08-246-427A-5 2 US-08-716-317-7 2 US-08-716-317-7 2 US-08-716-317-7 2 US-08-716-317-7 5 PCT-US93-06928-6 6 5186931-2	ALIGNMENTS	11-23 11-23 11-23 11-23 11-23 11-23 11-23 11-23 11-23 11-24 25 25 25 25 27 26 27 27 27 27 27 27 27 27 27 27 27 27 27	09230371A
16.6 16.5 16.5 16.5 16.5 16.5 16.5 16.5		ULT 1 Gegence 25, Application US/09230637 atent No. 6264958 APPLICANT: Harward, Gary APPLICANT: Harward, Gary APPLICANT: Harward, John APPLICANT: Hardwick, John APPLICANT: Reitz, Marvin TITLE OF INVENTION: No. 626495881 Genes FILE REFREENCE: 1007.78372 CURRENT FILING DATE: 1999-11-23 PRIOR APPLICATION NUMBER: 06/022,591 PRIOR FILING DATE: 1996-07-25 PRIOR FILING DATE: 1997-07-24 NUMBER OF SEQ ID NOS: 62 SOFWARE: PRAINT SHOWN VERSION 4 EQ ID NO 25 LENGTH: 204 TYPE: PRT ORGANISM: RAPOSI'S SATCOMA-ASSOCIATED A OP 230-230-637-25 USTY MATCH ORGANISM: RAPOSI'S SATCOMA-ASSOCIATED A OP 20-230-637-25 I MCWFKLWSLLLVGSLLVGGTRGKLPDAPE	-26 Application US/09230371A
28 182 330 181 331 181 332 181 334 181 335 181 34 181 440 181 441 181 45 181 45 181		1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	2 230-371A ence 26,
		RESULT 1 S-09-1 1 S-09-1 1 S-09-1 1 PRICE 1 APP 1 PRICE 1 PRIC	RESULT US-09- ; Sequ

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TYPE: amino acid
STRANDEDNESS: not relevant
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                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 185; Conservative
                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVHDK 204
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APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Moore, Patrick S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
FILE REPERBENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR PLING DATE: 1999-11-7
PRIOR PLING DATE: 1997-07-22
SUPPRIOR PLING DATE: 1997-07-22
SUPPRIOR PLING DATE: 1997-07-22
SUPPRIOR PLING DATE: 1997-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVI 120
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; Patent No. 6060264
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CUNTRY: California
COUNTRY: California
COUNTRY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1095; DB 3; Length 204; Best Local Similarity 100.0%; Pred. No. 3.5e-123; Matches 204; Conservative 0; Mismatches 0; Indels 0
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CUDNIKY: USAA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION: 436

PILING DATE: 24-UU.-1998

CLASSIPICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/053,765

FILING DATE: 25-UU.-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Kaposi's sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 EKFAGQAVRVLDSIPDVTPDVHDK 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRGKLPDAPEFEKDLLIGKLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 60
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TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCES. 16
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                     Length 185;
                                                                                                                                                                                                                                                                                                                                   90.6%; Score 992; DB 3; Length 18
100.0%; Pred. No. 7e-111;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 09/122,443
FILING DATE: cUnknown-
ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/558,089
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
DX0758K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-558-089-16; Sequence 16, Application US/09558089; Patent No. 6479634; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
                TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX. (650) 496-1200
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: not relevant
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61 TDHCGLIGFNETSCLKKLADGFPEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEE 120
                                                                                                                                                                                                       140 LNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVLDSIPDVTP 199
                                                                                                                                                                                                                          121 LNXLTKTHYSPPKFDRGLLGRLQGLKYWVRHPASFYVLSAMEKFAGQAVRVLDSIPDVTP 180
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                                                               1 TRGKLPDAPEPEKDLLIQRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 60
                                                                                                                          TDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEE
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TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 90.6%; Score 992; DB 4; L
Best Local Similarity 100.0%; Pred. No. 7e-111;
Matches 185; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/558,474
FILING DATE: 25-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
ULE TYPE: peptide
NCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/09558474
Patent No. 6835825
GENERAL INFORMATION:
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(650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 185 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                     200 DVHDK 204
                                                                                                                                                                                                                                                                                                                       DVHDK 185
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SEQUENCE
US-09-558-474-16
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                                                                                                                                                                                                                                                                                                                                                               LNKLTKTHYSPPKFDRGLIGRLQGLKYWVRHPASFVVLSAMEKFAGQAVRVLDSIPDVTP 199
                                                                                                                                                                                                                                                                                                                                                                                      80 TDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEE 139
                                                                                                                                                                                                     20 TRGKLPDAPEFEKOLLIQRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 79
                                                                                                                                                                                                                               TRGKLPDAPEFEKDLLIQRINWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 60
                                                                                                                                                               Gaps
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TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: 1
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.6%; Score 992; DB 4; Length 185; Best Local Similarity 100.0%; Pred. No. 7e-111; Matches 185; Conservative 0; Mismatches 0; Indels
                                                                                                                       90.6%; Score 992; DB 4; Length 185; 100.0%; Pred. No. 7e-111;
                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-UUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELEPRONE: (650)852-9196
TELEPRONE: (650)496-1200
                                                                                                                                  100.0%; Prea. ....
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APPLICATION NUMBER: US/09/558,087
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-09-558-089-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-087-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Patent No. 6495667
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 185 amino acids
TYPE: amino acid
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                                                                                                                                          Best Local Similarity 100.
Matches 185; Conservative
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| DVHDK 185
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88 FNETSCLKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTH 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPRWAEKDGCFQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 PEFEKDLLIQRIAWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 16.7%; Score 183; DB 1; Length 185; Best Local Similarity 25.6%; Pred. No. 1e-13; Matches 42; Conservative 38; Mismatches 84; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 YSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVL 191
                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
CUNTRY: United States
ZIP: 10014
COMPUTER: United States
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-UUL-1992
CLASSIFICATION: 435
|| :|| | ::: | : ::| :::| | 145 ASLLIKCLQAQNQWLQDMTTHLILRSFKEFLIRSLRAL 181
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Patent No. 5338833
GENERAL INFORMATION:
FAPLICANT: FOWLKES, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: Inclone Systems Incorporated
STREET: 180 Varick Street
                                                                                                                                                                                             GENERAL INFORMATION:
APPLICAMT: FOWNIES, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSS:
CARRESPENDENCE ADDRESSS:
CARRESPENDENCE ADDRESSS:
STREET: 180 Varick Street
                                                                                                                                                 Sequence 4, Application US/07918181A Patent No. 5338833
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NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 185 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: protein
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                 RESULT 8
US-07-918-181A-4
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US-07-918-181A-8
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                                                                                                                                                                                                                                                                          Sequence 12, Application US/08945529
Patent No. 5972902
Patent No. 5972902
GENERAL INFORMATION:
APPLICANT: CILIBERTO, Gennaro
APPLICANT: SAUTHO, ROCCO
APPLICANT: ANTAGONISTS OF HUMAN INTERLEUKIN-6 THAT
TITLE OF INVENTION: ANTAGONISTS OF HUMAN INTERLEUKIN-6 THAT
TITLE OF INVENTION: THE PREPARATION OF PHARMACEUTICAL COMPOUNDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
                                                  121 INXLIKTHYSPPKFDRGLIGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVLDSIPDVTP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 IDKQIRDILDFISALRKETCNKSNMCESSKEADAFWNLANDRWAEKDGCFYKGFNEETCL 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC compatible
COMPUTER: Pioppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,529
FILING DATE: 28-OCT-1997
CLASSIFICATION: 514
PRICK APPLICATION DATA:
APPLICATION NUMBER: IT RM95A000273
FILING DATE: 28-APR-1995
PRICK APPLICATION DATA:
FILING DATE: 28-APR-1995
PRICK APPLICATION NUMBER: PCT/IT96/00084
FILING DATE: 26-APR-1996
ATTORNEY AGENT INFORMATION:
NAME: YUN, Allen C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 RGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Suite 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 37,971
REPERENCE/DOCKET NUMBER: CI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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Matches 43; Conserv
                                                                                                                                                                181 DVHDK 185
                                                                                                                         DVHDK 204
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US-08-945-529-12
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REFERENCE/DOCKET NUMBER:
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US-08-231-575-8
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                                             COMPUTER FEDDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELEPHONE: 212-645-1405
TELEPAX: 212-645-1405
TELEPAX: 212-645-1405
TELEPAXION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TYPE: amino acid
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GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Muteins NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated STREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08231575
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United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42; Conservative
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Best Local Similarity
Matches 42; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-918-181A-8
COUNTRY:
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US-08-231-575-4
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88 FNETSCLKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTH 147
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                                                                                                                                                                                                                                                                                                                                                                      28 PEFEKDLLIQRINWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIG 87
                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                    Query Match 16.7%; Score 183; DB 1; Length 185; Best Local Similarity 25.6%; Pred. No. 1e-13; Matches 42; Conservative 38; Mismatches 84; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 YSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,575
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Inclone Systems Incorporated STREET: 180 Varick Street CITY: New York STATE: New York STATE: New York COUNTRY: United States ZIP: 10014 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08231575
Patent No. 5565336
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION:
C-Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inclone Systems Incorporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REPERENCE/DOCKET NUMBER: FOR
TELECOMMUNICATION:
TELEPHONE: 212-645-1405
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.7%;
25.6%;
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                    TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
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amino acid
                                                                                                                                                                                      / MOLECULE TYPE: protein US-08-231-575-4
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                                                               19 PLTSSERIDKQIRYILDGISALRKETCNKSNWCESSKEALAENNIALPYWAEKDGCFQSG 78
                                      28 PEFEKDLLIQRLNWMLWVIDBCFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIG 87
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Gaps
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16.7%; Score 183; DB 5; Length 185;
Best Local Similarity 25.6%; Pred. No. 1e-13;
Matches 42; Conservative 38; Mismatches 84; Indels
                                                                                                                                                                                                                               139 TPDPTTNASLLTKLQAQNQWLQDMTTHLILRSLKEFLQSSLRAL 182
                                                                                                                                                                                                     148 YSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVL 191
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rhes 84; Indels
84; Indels
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GENERAL INFORMATION:
APPLICANT: FOWNLESD, Dana M.
TITLE OF INTORNATION:
CORRESPONDENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCES: Inclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: PCT/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATYORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOW-2-T
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
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LENGTH: 185 amino acids
42; Conservative
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79 FNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAIT 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 PEFEKDLLIQRLNWMLWVIDBCFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIG 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.7%; Score 183; DB 5; Length 18 Best Local Similarity 25.6%; Pred. No. 1e-13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARES PATENTING STREET PURSON H1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: J3-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REFERENCE/DOCKET NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOW-2-T
TELECOMMUNICATION INFORMATION:
                                                 APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: Carboxy Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STRET: 180 Varick Street
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
Sequence 8, Application PC/TUS9306928 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 212-645-1405
212-645-2054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 185 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein PCT-US93-06928-8
                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                 COUNTRY: U.
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STATE: CA
COUNTRY: US,
ZIP: 91320
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US-08-792-019B-9
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58 GICKGILBPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGPFEFEVLFKFLTTEFGK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 IGLLLVLPAAFPAPPPGEDSKDVAAPHRQPLTSSERIDKQIRVILDGISALRKETCNKS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 VGSLLVSGTRGKLPDAP-EFEKDL------LIQRLNWMLWVIDECFRDLCYRT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 16.7%; Score 183; DB 1; Length 212; Best Local Similarity 25.8%; Pred. No. 1.3e-13; Matches 50; Conservative 38; Mismatches 92; Indels
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-PEB-1997
CLASSIFICATION: 514
ATTORNEY ACCURATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Comparible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/0898819;
Patent No. 6054294;
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN INC.
CITY: THOUSAND OAKS
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCS/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acids
STANDENNESS: single
                                                                                                                                                                                                                                              31,602
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MOLECULE TYPE: protein
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION:
US-08-792-019B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-988-819-9
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58 GICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                  16.7%; Score 183; DB 3; Length 212; ilarity 25.8%; Pred. No. 1.3e-13; Conservative 38; Mismatches 92; Indels
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COCK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/FOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
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196 RSFKEFLQSSLRAL 209
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                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                Protein
1..182
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Best Local Similarity
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LOCATION:
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US-08-988-819-9
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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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OM protein - protein search, using sw model Run on:

March 30, 2005, 21:49:40; Search time 172.897 Seconds (without alignments) 390.664 Million cell updates/sec

US-10-828-343-2 1095

1 MCWFKLWSLLLVGSLLVSGT..........GQAVRVLDSIPDVTPDVHDK 204 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

1407402 Total number of hits satisfying chosen parameters:

1407402 seqs, 331100923 residues

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Published_Applications_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMAKIES	
Result		Query	& Query	:	!	
NO.	Score	Match	Length	DB.	ID	Description
-	186	17.0	183	16	US-10-658-834A-927	
7	184	16.8	183	16	US-10-658-834A-901	
3	183	16.7	183	16	US-10-658-834A-900	
4	183	16.7	183	16	US-10-658-834A-918	
ς.	183	16.7	183	16	US-10-658-834A-920	Sequence 920, App
9	183	16.7	183	16	US-10-658-834A-928	
7	183	16.7	212	σ	US-09-854-280-14	Sequence 14, Appl
80	183	16.7	212	σ	US-09-854-208-14	Sequence 14, Appl
6	183	16.7	212	14	US-10-099-007A-3	Sequence 3, Appli
10	183	16.7	212	14	US-10-400-377-13	Sequence 13, Appl
11	183	16.7	212	14	US-10-400-708-13	Sequence 13, Appl
12	183	16.7	212	14	US-10-298-148-13	13,
13	183	16.7	212	15	US-10-440-464-61	Sequence 61, Appl

Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 906, App Sequence 918, App Sequence 918, App Sequence 918, App Sequence 918, App Sequence 914, App Sequence 917, App Sequence 917, App Sequence 912, App Sequence 922, App Sequence 922, App Sequence 922, App Sequence 923, App Sequence 939, App Sequence 939, App Sequence 134, App Sequence 163, App Sequence 164, App Sequence 164	Sequence 163, App Sequence 10, Appl Sequence 145, App Sequence 12, Appl Sequence 12, Appl Sequence 903, Appl Sequence 903, App Sequence 903, App Sequence 915, Appl Sequence 915, Appl Sequence 915, Appl Sequence 915, Appl
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ALIGNMENTS

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APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Ouyon, Thierry
APPLICANT: Drittenti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
TITLE OF INVENTION: Molecules and Related Applications
TITLE OF INVENTION: Molecules and Related Applications
FILE OF INVENTION: MOBER: US/10/658,834A
CURRENT APPLICATION NUMBER: US/10/658,834A
CURRENT APPLICATION NUMBER: 60/457,135
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 927
LENGTH: 183
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Sequence 927, Application US/10658834A Publication No. US20040132977A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: Gattler, Rene
APPLICANT: Gattler, Lila
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Or Lila
APPLICANT: Or INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding NucTITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A
CURRENT PILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR PILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE FARENCE: F
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                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                           16.7%; Score 183; DB 16; 125.6%; Pred. No. 2.5e-12; tive 37; Mismatches 85;
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                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.6%
Matches 42; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                  sapiens
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Best Local Similarity
Matches 42; Conserva
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; SEQ ID NO 900
; IENCTH: 183
; TYPE: PRT
; OKGANISM: HOMO S
US-10-658-834A-900
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US-10-658-834A-920
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Publication No. US20040132977A1

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-922
CURRENT FILING DATE: 2003-09-09

PRIOR FILING DATE: 2003-09-09

NUMBER OF SEQ ID NOS: 1306

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Publication No. US20040132977A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Guyon, Thierry

APPLICANT: Guyon, Thierry

APPLICANT: Oritication of Cytokines for Higher Stability, Encoding Nu

TITLE OF INVENTION: Molecules and Related Applications

FILE REPRENCE: 38751-922

CURRENT APPLICATION NUMBER: 60/457,135

PRIOR FILING DATE: 2003-09-09

PRIOR APPLICATION NUMBER: 60/409,898

PRIOR FILING DATE: 2002-09-09

NUMBER OF SEQ ID NOS: 1306

SOFTWARE: FASESQ for Windows Version 4.0
FNETSCLKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTH 147
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; Pred. No. 1.9e-12;
36; Mismatches 85;
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 43; Conserv
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US-10-658-834A-900
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APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Ui, Hanzhong
APPLICANT: Wood, William I.
TITLE OF INVENTION: IL-17 HOWOLGGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REPERENCE: P1381RLC2
CURRENT APPLICATION NUMBER: US 09/311,832
CURRENT APPLICATION NUMBER: US 60/085,579
FRIOR FILING DATE: 1999-05-14
FRIOR PILING DATE: 1998-05-15
FRIOR PILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 14
LENGTH: 212
TYPE: PRI
                                 58 GICKGILBPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFVLFKFLTTEFGK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 SVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVL 177
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       88 FNETSCLKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTH 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin
APPLICANT: Gurney, Austin
APPLICANT: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
TITLE OF INVENTION: THEREOF
FILE REPERBNCE: P1381-R1
CURRENT APPLICATION NUMBER: US/09/854, 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 212;
                                                                                                                                 148 YSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.7%; Score 183; DB 9; Length 21 Best Local Similarity 25.8%; Pred. No. 3e-12; Matches 50; Conservative 38; Mismatches 92; Indels
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                                                                                                                                                                                                                                                                            Sequence 14, Application US/09854280 Patent No. US20020052027A1
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US-09-854-280-14
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                                                             TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding NUTITLE OF INVENTION: Acid
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-92
CURRENT APPLICATION NUMBER: US/10/658,834A
CURRENT APPLICATION NUMBER: 06/457,135
PRIOR PILING DATE: 2003-09-09
PRIOR PILING DATE: 2003-09-09
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding NU
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
FILE REPERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A
CURRENT FILING DATE: 2003-09-08
PRIOR PILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 1306
SEQ ID NO 928
SEQ ID NO 928
LENGTH: 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FNETSCLKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTH 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.7%; Score 183; DB 16; Length 183; 25.6%; Pred. No. 2.5e-12; tive 37; Mismatches 85; Indels
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Publication No. US20040132977A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Gayon, Thierry
APPLICANT: Drittanti, Lila
Guyon, Thierry
Drittanti, Lila
Vega, Manuel
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US-10-658-834A-928
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Best Local Similarity
Matches 42; Conserva
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Best Local Similarity
Matches 42; Conserv
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196 RSFKEFLQSSLRAL 209
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Publication No. US20030017150A1

GENERAL INFORMATION:

APPLICANT: Theodore Torphy

TITLE OF INVENTION: CHRONIC OBSTRUCTIVE PULOMARY DISEASE-RELATED IMMUNOGLOBULIN

TITLE OF INVENTION: DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN-0286

CURRENT APPLICATION NUMBER: US/10/099,007A

CURRENT FILING DATE: 2002-03-14

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATENTIN VET 2.0

SOFTWARE: PATENTIN VET 2.0
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1 Similarity 25.8%; Pred. No. 3e-12;
50; Conservative 38; Mismatches 92; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.7%; Score 183; DB 14; Length 212; Best Local Similarity 25.8%; Pred. No. 3e-12; Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps
PRIOR APPLICATION NUMBER: US/09/311,832
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/085,579
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-12-13
PRIOR PILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 14
LENGRH: 212
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196 RSFKEFLQSSLRAL 209
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196 RSFKEFLQSSLRAL 209
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                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-208-14
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 50; Conserv
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US-10-099-007A-3
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| Sequence 11, Application US/1040377
| Sequence 11, Application US/1040377
| Sequence 11, Application US/1040377
| Sequence 11, Application No. US200301629481
| GEREBAL INFORMATION: | George N. |
| TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins |
| FILE OF INVENTION: Derivatives of Growth Hormone and Related Proteins |
| FILE OF INVENTION: DERIVATIVES OF Growth Hormone and Related Proteins |
| FILE OF INVENTION: DERIVATIVES OF Growth Hormone and Related Proteins |
| FILE OF INVENTION: DERIVATIVES OF GROWTH |
| FILE SEPREMENT: ADDITION: DERIVATIVES OF GROWTH |
| FILE SEPREMENT: ADDITION: DERIVATIVES OF GROWTH |
| FILE SEPREMENT: ADDITION: DERIVATIVES OF GROWTH |
| FILE SEPREMENT: DERIVATION OF GROWTH |
| FILE SEPREMENT: DERIVED OF GROWTH |
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TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
FILE REPERENCE: 038602/1592
CURRENT APPLICATION NUMBER: US/10/440,464
CURRENT PILING DATE: 2003-05-19
FRICA PAPLICATION NUMBER: 60/480,922
FRICA FILING DATE: 2002-05-17
FRICA FILING DATE: 2003-02-24
FRICA FILING DATE: 2003-02-24
FRICA FILING DATE: 2003-02-24
FRICA FILING DATE: 2003-02-24
FRICA REPERENCE: 2003-02-24
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FRICA REPERENCE: 2003-02-24
FRICA FILING DATE: 2003-02-24
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## APPLICANT: Cox III, George N
## APPLICANT: Cox III, George N
## APPLICANT: Bolder Biotechnology, Inc.
## APPLICANT: Bolder Biotechnology, Inc.
## TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
## TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
## CURRENT APPLICATION NUMBER: US/10/773,939
## CURRENT APPLICATION NUMBER: US/10/400,377
## PRIOR PAPLICATION NUMBER: US/10/400,377
## PRIOR PLING DATE: 2000-01-14
## PRIOR PLING DATE: 2000-01-14
## PRIOR PLING DATE: 1997-07-14
## NUMBER OF SEQ ID NOS: 41
## SOFTWARE: PatentIN Ver. 2.0
## SEQ ID NO 13
## LENGTH: 212
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; Publication No. US20040175356A1
; GENERAL INFORMATION:
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196 RSFKEFLQSSLRAL 209
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        SCHILLING, JIM
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US-10-440-464-61
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US-10-773-939-13
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                                                     118 SVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVL 177
--LIQRLNWMLWVIDECFRDLCYRT 57
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APPLICANT: COX III, George N
APPLICANT: Bolder Biotechnology, Inc.
ITILE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
ITILE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
CURRENT APPLICATION NUMBER: US/10/298,148
CURRENT FILING DATE: 2000-01-14
PRIOR PPLICATION NUMBER: US/09/462,941
PRIOR PPLICATION NUMBER: US/09/262,516
PRIOR PILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOPTHARE: Patentin Ver. 2.0
SEG ID NO 13
LENGTH: 212
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Best Local Similarity 25.8%; Pred. No. 3e-12;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps
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US-10-440-464-61
; Sequence 61, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRINO, SAMUEL
; APPLICANT: OF FARRELL; ANNE-MARIE
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: MANNING, WILLIAM
; APPLICANT: CHERRINGTON, JULIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12

US-10-298-148-13

US-10-298-148-13

Sequence 13, Application US/10298148

Publication No. US20030171284A1

GENERAL INFORMATION:
12 VGSLLVSGTRGKLPDAP-EFEKDL
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196 RSFKEFLQSSLRAL 209
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ORGANISM: Homo Bapiens
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58 GICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGK 117
                       177
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US-10-774-149-13

i Sequence 13. Application US/10774149

i Publication No. US20040175800A1

i GENERAL INFORMATION:

APPLICANT: COX III, George N

ITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

FILE REFERENCE: 415-1--90S

CURRENT APPLICATION NUMBER: US/10/774,149

CURRENT FILING DATE: 2003-03-26

FRIOR APPLICATION NUMBER: US/09/462,941

FRIOR PILING DATE: 2000-01-14

FRIOR FILING DATE: 2000-01-14

FRIOR FILING DATE: 1997-07-14

NUMBER OF SEQ ID NOS: 41

SEQ ID NO 13

LENGTH: 212
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196 RSFKEFLQSSLRAL 209
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CRGANISM: Homo sapiens
US-10-774-149-13
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5.1.6
Compugen Ltd.
GenCore version
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OM protein - protein search, using sw model

March 30, 2005, 21:47:50 ; Search time 48.4843 Seconds (without alignments) 404.837 Million cell updates/sec Run on:

US-10-828-343-2 Perfect score:

1 MCWFKLWSLLLVGSLLVSGT.......GQAVRVLDSIPDVTPDVHDK 204 Sequence:

283416 seqs, 96216763 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	interleukin-6 prec		kin 6	interleukin-6 prec	interleukin-6 - sh	ď		interleukin-6 prec	9	hypothetical prote	coenzyme F420-quin		DNA primase [impor	tubulin beta-1 cha	tubulin beta-5 cha	probable pheromone] ee	tubulin beta-1 cha	tubulin beta-7 cha		valine-tRNA ligase		beta-tubulin - pot	LRG1 protein - yea	ă	- 1	hypothetical prote	
SUMMARIES	QI	IVHUB2	I46590	146621	T09216	S29549	ICMS6	A56610	A34247	I46084	E90581	H69477	A56186	AG1256	UBMUBM	JQ1589	T41707	T18185	AC1619	500683	JQ1591	AB0985	F84972	S50747	S50748	S67804	T27626	JA0048	T19495	S04757
	Length DB	212 1		212 2				208 1					408 2	626 2	447 1	•	969 2	367 2		442 2			955 2				385 2			609 2
مد	Query Match Le	16.7	16.5	16.4		13.7	13.5	13.1	12.2	11.7	8.4	7.9	7.8	7.6	7.5	7.5	7.5	7.5	7.5	7.4	7.4	7.3	7.3	7.3	7.3	7.3	7.2	7.2	7.2	7.1
	Score	183	180.5	179.5	173.5	150	148	143.5	134	N	92.5	86.5	85	83	82.5	82.5	82.5	82	82	81.5	80.5	80	80	79.5	79.5		79	78.5	78.5	77.5
	Result No.	H	8	Ю	4	'n	ø	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote hypothetical prote resistance protein	tubulin beta chain tubulin beta chain protein kinase - f	sarcosine oxidase hypothetical prote	DNA-directed DNA p DNA gyrase, chain DNA gyrase subunit	probable rhol GDP- epididymal secreto	
S51421 B69483 T30562	S17729 S17730 T39889	B82969 T32824	D64246 C72043 H86579	T50454 A46695 R72364	B64380 S19169
0 0 0	0 0 0	000	0 0 0	0 0 0	124
771 1004 1810	447 447 461	1005	260 602 603	1158	333
7.1	7.0	0 0 0	, o, o,	0 0 0 0 8 8	9.8
77.5 77 77	76.5	75.5	75.5 75.5 75.5	75.5 75 75	75
3310	33 34 35	36 37	4 3 6 6 0	4 4 4 1 2 6	4 4 5

ALIGNMENTS

4	
1000	VHUB2

interleukin-6 precursor [validated] - human N;Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-cell

C;Species: Homo sapiens (man)
C;Species: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A35648; A25692; A2696; A33315; A25801; A25921; I52193; I56003; A27601; B27
R;Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishimot.
EMBO J. 6, 2939-2945, 1987
A;Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) gene
A;Reference number: A32648; MUID:88082664; PMID:3500852

A; Accession: A32648

A, Molecule type: DNA
A, Residues: 1-212 < YAS>
A, Residues: 1-212 < YAS>
A, Residues: 1-212 < YAS>
A, Cross tracerences UNIPROT: P05231; GB: Y00081; NID: 929494; PIDN: CAA68278.1; PID: 929495
A, Note: the authors translated the codon CAG for residue 130 as Glu
R, Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
EMBO J. 5, 2529-2337, 1986
A, Title: Structure and expression of CDNA and genes for human interferon-beta-2, a distinal streets number: A91051; MUID: 87053818; PMID: 3023045

AjAccession: A26966
AjMolecule type: mRNA
A;Residues: 1-212 - 4HR>
A;Cross-references: GB:X04602; NID:g33849; PIDN:CAA28268.1; PID:g33850
R;Tonouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.
Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
A;Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization of A;Reference number: A33515; MUID:89391958; PMID:2789513

A; Molecule type: mRNA A; Residues: 1-212 <TON>

A;Cross-references: GB:M29150; NID:g186349; PIDN:AAA59154.1; PID:g307063
R;Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.; (Tavernier, J.; Fiers, W.
Eur. J. Biochem. 159, 625-632, 1986
A;Title: Structural analysis of the sequence coding for an inducible 26-kDa protein in h
A;Reference number: A25801; MUID:87004683; PMID:3758081

A; Molecule type: DNA; mRNA

A,Residues: 1-212 <HAE>
A,Cross-references: GB:X04403
A,Experimental source: fibroblast
R;May, L.T.; Helfgott, D.C.; Sehgal, P.B.

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50; Conservative
                                                                                                                                           A; Molecule type: protein
                                                                                                                                                                                        A;Residues: 28-40 <MAY3>
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Approcession: 156003
Approcess
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Moda, M.; Takda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; Az
Anticancer Res. 11, 961-968, 1991
A;Title: Purification and characterization of human fibroblast derived differentiation i
A;Reference number: A61159; MUID:91290785; PMID:1648338
A;Molecule type: protein
A;Residues: 30-42 <NOD>
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R;Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno, A.
Mol. Cell. Immunol. 4, 203-212, 1989
A;Title: Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor fc
A;Reference number: A61462; MUID:90121567; PMID:2610854
Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
A;Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
A;Reference number: A25921; MUID:87067433; PMID:3538015
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A; Molecule type: protein
A; Residues: 28-48 cMIN.
A; Experimental source: leukocyte-conditioned medium
B; May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal, P.B.
Cytokine 3, 204-211, 1991
A; Title: Marked cell-type-specific differences in glycosylation of human interleukin-6.
A; Reference number: A48419; MUID:91355644; PMID:1883960
                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-212 < rAAY>
A; Residues: 1-212 < rAAY>
A; Cross-references: CB:M14584; NID:g184628; PIDN:AAA52728.1; PID:g306910
R; Wong, G.G.; Witek-Giannotti, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
Behring Inst. Mitt. 83, 40-47, 1988
A; Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
A; Reference number: I52193; WUID:89193317; PMID:3266463
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A;Residues: 30-37,'X',39-40 <MAY2>
A;Experimental source: FS-4 fibroblasts
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A; Experimental source: FS-4 fibroblasts
A; Experimental source: FS-4 fibroblasts
A; Note: this 23-25K form contained O-linked but not N-linked carbohydrate
A; Note: this 23-25K form contained O-linked but not N-linked carbohydrate
B; Orita, T.; Oheda, M.; Hassgawa, M.; Kuboniwa, H.; Esaki, K.; Ochi, N.
J. Biochem. 115, 345-350, 1994
A; Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 product A; Contents: annotation; modified sites in recombinant protein from CHO cells
A; Chorents: annotation; modified sites in recombinant protein from CHO cells
R; Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
A; Title: Disulfide structures of human interleukin-6 are similar to those of human granul A; Reference number: S04981; MUID: 89286115; PMID: 2472117
A; Contents: annotation; disulfide bonds in recombinant protein
R; Rock, F.L.; Li, X.; Chong, P.; Ida, N.; Klein, M.
Biochemistry 33, 5146-5154, 1994
A; Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
A; Reference number: A54253; MUID: 94227044; PMID: 8172889
A; Contents: annotation; lability and functional significance of each disulfide bond C; Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth factors (Comment: This protein plays a regulatory role in various host defense mechanisms and er C; Genetics:
A; Chose. Tobasines. Charles One 100 A; Contents and er C; Comment: This protein plays a regulatory role in various host defense mechanisms and er C; Genetics:
A; Chose. Tobasines. Charles One Charles On
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Aintrons: 7/1; 70/3; 108/3; 157/3
C.Superfamily: interleukin-6
C.Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growth fa
A;Note: sequence extracted from NCBI backbone
A;Note: this 28-30K form contained both N-linked and O-linked carbohydrate; a 25K form cc
A;Accession: C48419
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F;28-212/Product: interleukin-6, long form #status experimental <MATL>
F;28-212/Product: interleukin-6, short form #status experimental <MATS>
F;30-212/Product: interleukin-6, short form #status experimental <MATS>
F;72-79,101-111/Disulfide bonds #status experimental
F;73/Binding site: carbohydrate (Ann) (covalent) (partial) #status experimental
F;166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
F;172/Binding site: carbohydrate (Ann) (covalent) #status predicted
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: Sus scrofa domestica (domestic pig)
C;Accession: I46590
R;Mathialagan, N.; Bixby, J.; Roberts, M.R.
MOI. Reprod. Dev. 32, 324-330, 1992
A;Fitle: Expression of interleukin-6 in porcine, ovine, and bovine preimplan
A;Reference number: I46590; MUID:92360284; PMID:1497880
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Pred. No. 5.5e-10;
8; Mismatches 92; Indels
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25.8%; Pred. No. ...
... 38; Mismatches
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19;

Length 208; Indels

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61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 NIKTMQISTKVL---VQILMQKMKNPEVTTPDPTAKSSLLAKKHSQNEWLKNTTHLILR 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| || | | : :: | | : :: | | : :: | | : :: | | : :: | | : :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | ::
                                                                                                                                                                                            A;Accession: T09216
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule 'type: mRNA
A;Residues: 1-208 <SMI>A;Residues: 1-208 <SMI>A;Cross-references: UNIPROT: Q95181; EMBL: U64794; NID: 92654387; PID: 92654388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin-6 - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: S2549
R;Ebrahimi, B.
Submitted to the EMBL Data Library, October 1992
A;Reference number: S29549
A;Reference number: S29549
A;Reference preliminary
A;Reference to the EMBL Data Library, October 1992
A;Reference number: S29549
               C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.8%; Score 173.5; DB 326.0%; Pred. No. 4.3e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
15.8%; Score 173.5; Best Local Similarity 26.0%; Pred. No. 4.3e Matches 51; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: UNIPROT: P29455; EMBL: X68723 C, Superfamily: interleukin-6
                                                      C;Accession: T09216
R;Swiderski, C.E.; Horohov, D.W.
Bubmitted to the EMBL Data Library, July 1996
A;Reference number: Z16613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 AKVIIILRSLENFLQFRLRAI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 FASFYVLSAMEKFAGQAVRVL 191
                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: IL-6
C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 SLEDFLQFSLRAVRIM 208
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-212 < MMT>
A;Cross-references: UNIPROT:P26893; GB:M80258; NID:g164514; PIDN:AAC27127.1; PID:g164515
C;Genetics:
A;Genetics: L1-6
C;Superfamily: interleukin-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gross-references: UNIPROT:P26893; GB:M86722; NID:g164624; PIDN:AAC37333.1; PID:g164629
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prointerleukin 6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: 146621
R;Richards, C:; Saklatva, J.
C;Yrokine 3, 269-276, 1991
A;Richards 1, 269-276, 1991
A;Reference number: 146621; MUID:91338547; PMID:1873476
A;Recession: 146621
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-212 <RIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: | | : | | : | | : | | EKCENSKEVLAENDILPKWAEKDGCFQSGFNQETCLMRITTGLVEFQIYLDYLQKEYES 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 GICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVINVDVMBLLITKTLGWDIQEBLNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 CYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTT 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGLLLVMATAPPPERLEEDAKGDATSDKMLFTSPDKTEBLIKYILGKISAMRKEMCEKY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 VGSLLVSGTRGKLPDAPEFE------KDLLIQRLNWMLWVIDECFRDLCYRT 57
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                                                                                                                                                                                                                                                                                                                 Length 212;
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                                                                                                                                                                                                                                                                                                                                                                                    87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79; Indels
                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                          16.5%; Score 180.5; DB 2 23.9%; Pred. No. 9.5e-10; ive 46; Mismatches 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAME --- KFAGQAVRVL 191
                                                                                                                                                                                                                                                                                                                                                                                    47; Conservative
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C,Superfamily: interleukin-6
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Matches 48; Conserv
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interleukin-6 precursor - mouse N;Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocy

interleukin-6 precursor - horse C, Species: Equus caballus (domestic horse)

4; Gaps

71; Indels

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A;Map position: 5
A;Introns: 7/1; 68/3; 106/3; 156/3
C;Superfamily: interleukin: 5
C;Superfamily: interleukin: growth factor; immunoregulation; lymphokine; n
C;Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; n
F;1-24/Domain: aignal sequence #status predicted <SIG>
F;25-211/Product: interleukin-6 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:g581860
R;Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
Eur. J. Bloochem. 217, 53-59, 1993
A;Title: Specific covalent modification of the tryptophan residues in murine interleukin. A;Reference number: S38254; MUID:94039075; PMID:8223586
A;Accession: S38254
A;Status: preliminary
A;Residues: preliminary
A;Residues: 38-60;75, X', 77-79;176-203 <ZHA>
RiBlankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A;Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a mou
A;Reference number: S10241; MUID:90171860; PMID:2106569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 KKDKARVLQRDTETLIHIFNQEVKDLHKIVLPTPISNALLTDKLESQKEWLRTKTIQFIL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 VGSLLVSGT-----RGKL-----PDAPEFEKDLLIQRLNWMLWVIDECFRDLCYRTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 148; DB 1;
Pred. No. 1.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.5%; Sco. No. 1.2.
24.5%; Pred. No. 1.2.
've 35; Mismatches
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Best Local Similarity
Matches 47; Conserva
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es 42; Conserva
                                                                                                                                                                         A, Accession: S10241
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-6 < SLA>
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A,Gene: Il-6
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A; Residues: 25-166,'X',168-211 <SIM>
A; Residues: 25-166,'X',168-211 <SIM>
A; Residues: 25-166,'X',168-211 <SIM>
A; Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A
R; Grenett, H.E.; Fuentes, Ni.; Fuller, G.M.
Nucleic Acids Res. 18, 6455, 1990
A; Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
A; Reference number: $12103; MUID:91057159; PMID:2243807
A; Accession: $12103
A; Molecule type: mRNA
    acytoma growth factor
Cispecies: Mus musculus (house mouse)
Cjoate: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
CjAccession: A30531; A27610; A30571; S01322; S12103; E34047; A26662; A40486; A60799; S16
R;Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
J. Immunol. 141, 3875-3881, 1988
A;Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential
                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-211 <TAN's
A; Cross-references: UNIPROT: P08505; GB: M20572; NID: g198369; PIDN: AAA39302.1; PID: g387386
A; Cross-references: UNIPROT: P08505; GB: M20572; NID: g198369; PIDN: AAA39302.1; PID: g387386
R; Van Snick, J.; Cayphas, S.; Saikora, J.P.; Renauld, J.C.; Van Roost, E.; Boon, T.; Sim
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Exp. J. Immunol. 18, 193-197, 1988
A; Title: CDNA cloning of murine interleukin-HP1: homology with human interleukin 6.
A; Reference number: A27610; MUID: 88166883; PMID: 2965020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Mesidues: 1-211 cVAN.
A; Cross-references: GB:X06203; NID:952701; PIDN:CAA29560.1; PID:952702
A; Cross-references: GB:X06203; NID:952701; FIDN:CAA29560.1; PID:952702
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A; Timunol. 142, 1372-1376; 1989
A; Title: The murine II-6 gene maps to the proximal region of chromosome 5.
A; Reference number: A30571; MUID:89124383; PMID:2563387
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R;Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
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A;Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage A;Reference number: A90157; MUID:90147691; PMID:2302197
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A;Molecule type: protein
R;Rseadues: 66-66,7x',71-75;78-94;128-148 <785>
R;Rseadues: 66-66,7x',71-75;78-94;128-148 <785>
R;Van Snick, J.; Cayphas, S.; Vink, A.; Uyttenhove, C.; Coulie, P.G.; Rubira, M.R.; Simp Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
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A;Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokin A;Reference number: A26662; MUID:87092311; PMID:2948184
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A;Molecule type: protein

B;Rebidues: 25-39,'X',41-42,'X',44-45 <VSN>

R;Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.

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A;Reference number: A40486; MUID:89017145; PMID:3262872
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A; Residues: 1-211 «CH1>
A; Cross-references: GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410
A; Cross-references: GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410
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Blood 72, 2070-2073, 1988
A; Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6
A; Reference number: A60799; MUID:89062753; PMID:3264198
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R;Simpson, R.J.; Moritzz, R.L.; Rubira, M.R.; Van Snick, J.
Eur. J. Biochem. 176, 187-197, 1988
A;Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and A;Reference number: S01323; MUID:88329059; PMID:3262059
Ä;Molecule type: nrotot-
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A; Molecule type: mRNA
A; Residues: 5-211 <MOC>
A; Cross-references: GB:N
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A;Residues: 1-211 <GRE>
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Gaps

96; Indels 14;

28

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A;Residues: 1-208 <DRO>
A;Cross-references: UNIPROT:P26892; EMBL:X57317; NID:g2193; PIDN:CAA40572.1; PID:g2194
A;Cross-references: UNIPROT:P26892; EMBL:X57317; NID:g2193; PIDN:CAA40572.1; PID:g2194
A;Cxoss-references: BLV induced B cell-lymphosarcoma
A;Note: sequence extracted from NCBI backbone (NCBIP:118917)
C;Superfamily: interleukin-6
C;Keywords: cytokine
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interleukin-6 precursor - bovine
C;Species: Bos primidgenius taurus (cattle)
C;Species: Bos primidgenius taurus (cattle)
C;Accession: A56610; 822162
C;Accession: A56610; 822162
R;Droogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
DNA Seq. 2, 411-413, 1992
A;Fitle: Nucleotide sequence of bovine interleukin-6 cDNA.
A;Fitle: Nucleotide sequence of bovine interleukin-6 cDNA.
A;Accession: A56610
A;Status: A56610
A;Status: preliminary
A;Molecule type: MANA
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24.4%; Pred. No. 3.2e-06;
tive 37; Mismatches 86
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A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-6 precursor - rat
NyAlternate names: IL-6
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Uun-1990 #sequence_revision 15-Uun-1990 #text_change 09-Jul-2004
C;Accession: A34247
C;Accession: A34247
C;Accession: A34247
C;Accession: A34247
A;Reference number: A34247; MUD:89380206; PMID:2789217
A;Reference number: A34247
A;Accession:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-211 <NOR>
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C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage
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A;Cross-references: UNIPROT:P41683; GB:L16914; NID:g438519; PIDN:AAA16620.1; PID:g438520
C;Superfamily: interleukin-6
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C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
R;Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
Proc. Soc. Exp. Biol. Med. 204, 301-305, 1993
A;Title: Molecular cloning and characterization of a cDNA encoding feline interleukin-6.
A;Reference number: 146084
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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                                                                                TDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEE 139
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41 TPGRLLLTTPEKTEALIKR----MVDKISAMRKEICEKNDECESSKETLAENKINLPKMEE 97
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189 TIQLILKALEEFLKVTMR 206
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Matches 47;
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4 FKLWSLLLV-----GSLLVSGTRGKLPDAPEFEKDLLIQRLNWMLWVIDECFRDLCYR 56

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R;Chambaud. 1.7 Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulme A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: E90581
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-873 «KUR»
A;Cross-references: UNIPROT:Q98Q12; GB:AL445566; PID:g14089972; PIDN:CAC13730.1; GSPDB:G:
A;Experimental source: strain UAB CTIP
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NyAlternate names: F420H2-quinone oxidoreductase, 53.9K subunit nuoM homolog
Cippecies: Archaeoglobus fulgidus
Cippecies: Archaeoglobus fulgidus
Cipacession: H69477
Rixlenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson
FRixlenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson
Frischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
Alauthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.;
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo.
A;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein MYPU 5570 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Species: Mycoplasma pulmonis C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ģ
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                                                                                                                                                                                  11 YNKCEDSKEALAENNLALPKLAEKDGCFQSGFNQETCLTRITTGLQEFQIYLKFLQDKYE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 SCLKKLADGFFEFEVLF-----KFLTTEFCKS-VINVDVMELLTKTLGWDIQ---- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 AKEKGVEISLEEFEKYRQEHELKSKSKKGDGMKKVINFLANIDKKVDEFVGYDTLETTSK 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: H69477
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-487 < KLE>
14 FSLGLLLVVATARPTPGPLGGDATSNRLPLTP---ADKMEELIKYILGKISALKKEMCDN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EELNKLTKTHYSPPKFDRG----LLGRLQGLKYWVRHFASFYVL----
                                                                                                                               57 TGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 KOLLIQRINWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 873;
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                                                                                                                                                                                                                                                                                                        116 ----GKSV-INVDVMELLTKTLGWDIQEEL 140
                                                                                                                                                                                                                                                                                                                                                           ||| : :|: : | : |:|:
131 GDKENAKSVYTSTNVLLQMLKRKGKN-QDEV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

8.4%; Score 92.5; Di
Best Local Similarity 24.3%; Pred. No. 1.3;
Matches 50; Conservative 27; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: alanyl-tRNA ligase
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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Adcession: Ad226
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Accussion: AG1256
A;Actus: preliminary
A;Adlecule type: DA7A
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A;Cross-references: UNIPROT:P47762; GB:NC_003210; PIDN:CAC99533.1; PID:g16410884; GSPDB:C
A;Experimental source: strain EGD-e
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-447 < COPP>
A; Cross-references: UNIPROT: PI2411; GB: M20405; NID: 9166921; PIDN: AAA32893.1; PID: 9166922
A; Note: the genome of A. thaliana contains a beta-tubulin gene family consisting of at 16
A; Note: the transcript of this beta-1 tubulin gene accumulates predominantly in roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tubulin beta-1 chain - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: 470275
R;Oppenheimer, D.G.; Haas, N.; Silflow, C.D.; Snustad, D.P.
R;Oppenheimer, D.G.; Haas, N.; Silflow, C.D.; Snustad, D.P.
A;Title: The beta-tubulin gene family of Arabidopsis thaliana: preferential accumulation
A;Reference number: JT0275; MUID:88255862; PMID:3384336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 GTLLVERNRLDVFVLQLPAGKDPDPIRASGPEKFKEVYKQQRMTWTAFKIHYLRKERNL 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387 Q------NETEQIGYI----DDCLREIAKLDQAVERELYLKQLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 RTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLA--DGFFEFEVLFKFLTT
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C;Superfamily: tubulin
C;Keywords: microtubule
F;141-147/Region: tubulin/FtsZ GTP/GDP-binding (G-G-G-T-G-[ST]-G) motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 EFGKSVINVDVMELLTKTLGWDIQEELNKLTKTH----YSPPKFDRGLLGRL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422 EF-----ELTIETLKQQLQOSLKNSQKSRQMASYNEPPIDDSFMGMM 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%; Score 83; DB 2;
23.8%; Pred. No. 7;
tive 21; Mismatches 5;
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NyAlternate names: cyclin E1

C,Species: Xenopus lasvis (African clawed frog)

C,Species: Xenopus lasvis (African clawed frog)

C,Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 12-Jul-2004

C,Accession: A56186; S34125

R;Rempel, R.E.; Sleight, S.B.; Maller, J.L.

J. Biol. Chem. 270, 6843-6855, 1995

A;Title: Maternal Xenopus Cdk2-cyclin E complexes function during meiotic and early embra A;Recference number: A56186; MUID:95204484; PMID:7896832

A;Reference number: A56186, MUID:95204484; PMID:7896832

A;Residus preliminary

A;Molecule type: mRNA

A;Residus: J-408 <RENA

A;Coss-references: UNIPROT:Q91780; GB:L23857; NID:9431745; PIDN:AAA73524.1; PID:9431746

R;Couturier, A.; Philippe, M.

Submitted to the EMBL Data Library, June 1992

A;Reference number: S34125

A;Reference number: S34125

A;Reference number: S34125
A;Cross-references: UNIPROT:028450; GB:AE000976; GB:AE000782; NID:g2689299; PIDN:AAB8942
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: oxidoreductase
                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                   ::|| | | :: : | 263 YMIDSSFIDQYRDIIAYAIVSSIYAGFSVFKQK-----DYKRLLAYSTVSQMGYVLI 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 PQFPQEIYIQ----IVQLLDLCVLDIC----CLEYPYGVLAASAMYHFSCPELVEK--- 314
                                                                                                                                                                                                                                                                                                     FTAWLLIFLGMLV-----KLFGLGPHIWLPWAHAEAPTPVSALLSPLTVGLAGYVLLRV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 --CLKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTH-YS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 -VSGFKVTELQGCIKWL-----VPFAMAIKEGGKSKLNFFKGVDIEDAHNIQTHSGC 365
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                                                                                                                                                                                                                                               -DAPEFEKDLL----IQRLNWML---
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                                                                                                                                                                                                                                                                                                                                                            WVIDECF----RDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETS-----
                                                                                                                                                                                        Gaps
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                                                                                                                               Length 487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 PPKFDRGLLG--RLQGLKYWVRHFASFYVLSAMEKFAGQAVRVL 191
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DNA primase [imported] - Listeria monocytogenes (strain EGD-e)
                                                                                                                                                                                  79; Indels
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A;Molecule type: mRNA
A;Residues: 1-32, 'A', 34-199,'NV',202-258,'GN',261-408 <COU>A;Coss-references: BMBL;Z13966
C;Superfamily: cyclin, A/B/D/E type
C;Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                         DB 2;
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                                                                                                                         7.9%; Score 86.5; DE 21.4%; Pred. No. 2.4; rative 40; Mismatches
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Matches 37; Conservative
                                                                                                                         Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                        209
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Gaps

58;

52; Indels

Length 626;

22

113 421 ä

Gaps

49; Indels

DB 1; Length 447;

49

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RESULT 15
JQ1589
tubulin beta-5 chain - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dete: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JQ1589
R;Snustad, D.P.; Haas, N.A.; Kopczak, S.D.; Silflow, C.D.
R;Snustad, D.P.; Haas, N.A.; Kopczak, S.D.; Silflow, C.D.
A;Title: The small genome of Arabidopsis contains at least nine expressed beta-tubulin g
A;Accession: JQ1589
A;Accession: JQ1589
A;Accession: JQ1589
A;Residues: 1-449 <SNU>
A;Residues: 1-449 <SNU>
A;Coss-references: UNIPROT:P29513; GB:M84702; NID:g166901; PIDN:AAA32883.1; PID:g166902
C;Genetics:
A;Gene: TUB5
C;Keywords: microtubule
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255 AVNLIPPPRLHFFMVGFAPLTSRGSQQYISLTVPELTQQM--WD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 ADGFFEFEVLFKF-----LITTEFGKSVINVDVMELLTKTLGWD 135
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Search completed: March 30, 2005, 22:06:42 Job time : 50.4843 secs

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GenCore version 5.1,6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

March 30, 2005, 21:12:44; Search time 214.063 Seconds (without alignments) 488.007 Million cell updates/sec

US-10-828-343-2 1095

1 MCWFKLWSLLLVGSLLVSGT........GQAVRVLDSIPDVTPDVHDK 204 Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

ption	human herne				saimiri sci	cercocebus	homo sapien		macaca mula	sus scrofa	aotus nancy	sus scrofa	equus cabal	felis silve	lama glama	sus scrofa	phoca vitul	delphinapte	camelus bac	orcinus orc	gallus gall	canis famil	capra hircu	ovis aries	mus musculu	canis famil	bos taurus	aotus nigri	bubalus bub	marmota mon	enhydra lut
Description	098823	0768k3	040918	P79341	Q8mkh0	P46650	P05231	Q9tth3	P51494	P26893	097540	Q8m j 75	095181	P41683	Q865x6	Q8mke5	028819	09xt80	Q865w7	028747	Q90y10	O9myz7	028319	P29455	P08505	P41323	P26892	Q9tth4	Q6v919	Q9jhh3	Q28403
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SUMMAKIES	098823	Q76SK3	040918	IL6 MACFA	Q8MKH0	IL6 CERTO	IL6 HUMAN	ооттн3	IL6_MACMU	IL6_PIG	097540	Q8MJ75	IL6 HORSE	IL6 FELCA	IL6 LAMGL	Q8MKE5	IL6 PHOVI	Q9XT80	Q865W7	IL6 ORCOR	Q90 <u>Y</u> 10	CSWYZ7	IL6_CAPHI	IL6_SHEEP	IL6_MOUSE	IL6_CANFA	IL6 BOVIN	Q9TTH4	Q6V919	Фэлниз	Q28403
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% Query Match	100.0	100.0	99.4	16.9	16.8	16.7	16.7	16.6	16.5	16.5	16.3	16.2	15.8	14.9	14.8	14.6	14.6	14.4	14.4	14.2	14.2	14.1	13.9	13.7	13.5	13.2	13.1	13.1	12.7	12.6	12.5
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ALIGNMENTS

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61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFBVLFKFLTTEFGKSVI 120
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                                                                                                            Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
Viruses, dBDM viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
NCBI_TaxID=37296;
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                                                                                                                                                                                         SEQUENCE FROM N.A.
Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,
Friedman-Kien A.-E., Fleckenstein B.;
"Human herpesvirus B encodes a homologue of interleukin-6.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 204 23408 MW; 1CA7772A0EDCO5EB CRC64;
                                                                                                                                                                                                                                                                                                    GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; IL6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
                            01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Interleukin-6 homolog (Fragment).
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100.0%; Score 1095; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.4e-92;
Matches 204; Conservative 0; Mismatches 0;
 204 AA
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 PRT;
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PRINTS; PR00434; INTERLEUKING.
PRODOM; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
NON TER 204 204
SEQÜENCE 204 AA; 23408 MW; ICA7
                                                                                                                                                                                                                                                         J. Virol. 0:0-0(1996).
EMBL; U73655; AAB18244.1; -.
PRELIMINARY;
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Length 204;

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01-JAN-1998 (TrEMBLrel. 05, 01-OCT-2001 (TrEMBLrel. 18,
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"A single 13-Kilobase divergent locus in the Kaposi sarcoma-associated herpesvirus (human herpesvirus 8) genome contains nine open reading frames that are homologous to or related to cellular proteins.";
J. virol. 71:1963-1974(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D., Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.; Submitted (WAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U71365; AAC34937.1; --
EMBL; U71365; AAC34937.1; --
EMBL; U71569; AAC37089.1; --
EMBL; U75698; AAC37089.1; --
EMBL; U75698; F:cytcacellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
GO; GO:0005139; F:interleukin-6 receptor binding; IEA.
InterPro; IPR003579; IEG MGF GCSF.
InterPro; IPR003574; Interleukin-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDILINES97208913; PubMed=9055855;
MEDILINES97208913; PubMed=9055855;
Nicholas J., Ruvolo V.R., Burns W.H., Sandford G., Wan X., Ciufo D., Hendrickson S.B., Guo H.G., Hayward G.S., Reitz M.S.;
"Kaposi's sarcoma-associated human herpesvirus-8 encodes homologues of macrophage inflammatory protein-1 and interleukin-6.";
Nat. Med. 3:287-292(1997).
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
NCBI_TaxID=37296;
                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
08-JUL-2004 (TrEMBLrel. 27, Last annotation update)
0RF K2; functional interleukin-6 vIL-6 homolog (Putative interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97094384; PubMed=8939871; DOI=10.1126/science.274.5293.1739; Moore P.S., Boshoff C., Weiss R.A., Chang Y.; "Molecular minicry of human cytokine and cytokine response pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97121480; PubMed=8962146; DOI=10.1073/pnas.93.25.14862; Messo JJ., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.; "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-97184526; PubMed-9032328;
Nicholas J., Ruvolo V., Zong J., Ciufo D., Guo H.G., Reitz M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sun R., Lin S.-F., Miller G.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                            204 AA
181 EKFAGQAVRVLDSIPDVTPDVHDK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
SEQUENCE 204 AA; 23408 MW; 1CA7
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PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
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                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neipel F., Albrecht J.C., Fleckenstein B.; "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus human herpesvirus 8: determinants of its pathogenicity?"; J. Virol. 71:4187-4192(1997).
                                                                                                                                                          1 MCWFKLWSLLLVGSLLVSGTRGKLPDAPEFEKDLLIQRLNWMLWVIDECFRDLCYRTGIC
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Neipel F., Albrecht J.C., Ensser A., Huang Y.Q., Li J.J., Arlodman-Kien A.E., FleckRensteln B.;
"Human herpesvirus 8 encodes a homolog of interleukin-6.";
J. virol. 71:839-842(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
100.0%; Score 1095; DB 2;
100.0%; Pred. No. 2.4e-92;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.4%; Score 1088; DB 2; 99.0%; Pred. No. 1.1e-91; tive 2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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PRINTS; PRO0434; INTERLEUKING.
PRODOM; PD004356; Interleukin_6; 1.
SWART; SM00126; ILG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 EKFAGQAVRVLDSIPDVTPDVHDK
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MEDLINE=97296220; Pubmed=9151804;
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14; Gaps

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58 GICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGK 117
                                                                       LGLLLVLPAAFPAPVLPGEDSKDVAAPHSQPLTSSERIDKHIRYILDGISALRKETCNRS
                                              12 VGSLLVSGTRGKLPDAP-EFEKDL------LIQRLNWMLWVIDECFRDLCYRT
Pred. No. 8.2e-09;
                    51; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                    PRT;
         26.3%;
                                                                                                                                                                                                                                 196 RSFKEFLQSSLRAL 209
                                                                                                                                                                                                         178 SAMEKFAGQAVRVL 191
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Now. Ited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                            KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVI 120
                                                                                               NVDVMELLIKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAM 180
                                                                                                              NYDVMELLIKTLGWDIQEELNKLIKTHYSPPKFDRGLIGRLGCIKYWVRHFASFYVLSAM 180
                                            KGILBPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVI 120
    6.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, hepatocytes it induces acute phase reactants (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and expression of cynomolgus monkey interleukin-
                                                                                                                                                                                                                                                                                                                                     Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
CF8173FCBF0B0389 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                     15-UUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                              212 AA
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By similarity.
By similarity.
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InterPro; IPR003573; II6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PP00489; II6; 1.
                                                                                                                                                                EKFAGQAVRVLDSIPDVTPDVHDK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0433; ILGGCSFMGF.
PRINTS; PRO0434; INTERLEDKING.
PRO0400; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                             Interleukin-6 precursor (IL-6).
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acute phase;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ratsumi M.;
                                                                                                                                                                                                                                            IL6 MACFA P79341;
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118 SVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLGGLKYWVRHFASFYVL 177
                                                                                          116 GKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFY 175
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:::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| 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Immunogenetics 54:20-29(2002).
EMBL; AF294757; AAK92044.1; -.
HSSP; P05231, ILL6.
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Bukaryota: Metazoa (Chordata; Craniata: Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
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MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;
Heraud J.M., Lavergne A., Kazanji M.;
"Molecular cloning, characterization, and quantification of squir
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Local Similarity 25.3%; Pred. No. 1e-08;
Ags 50; Conservative 40; Mismatches وع. تسطماء
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PRINTS; PR00414; INTERLEUKIN6.
PRODOM; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; I. InTERLEUKIN 6; 1.
SROOTTB; PS00254; INTERLEUKIN 6; 1.
SEQUENCE 212 AA; 23581 MW; PF22CBF493245479 CRC64;
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GO; GO:000518; F:cytokine activity; IEA.
GO; GO:0005138; F:cytokine activity; IEA.
GO; GO:0006955; P:inmune response; IEA.
InterPro; IPR00979; 4 Helix Cytokine.
InterPro; IPR003573; IL6 MGF GGSF.
InterPro; IPR003574; Interleukin.6.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Biochem. Biophys. Res. Commun. 163:1056-1062(1989)
                                                                                          196 RSFKEFLQSSLRAL 209
                                                                 178 SAMEKFAGQAVRVL 191
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                                                                                                                                                                                                                                                                   Name=IL6; Synonyms=IFNB2;
                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
                                                                                                                                                                                                                                                       (CDF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene.
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                                                                                                                                                            LE HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2/IL-6)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 GICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPhvo.

A InterPro; IPhvo.

InterPro; IPhvo.

B Fam; PF00489; IL6; 1.

DR PRINTS; PR00431; IL6GCSFMGF.

DR PRINTS; PR00434; INTERLEUKING.

DR PRODOM; PD004356; Interleukin_6; 1.

DR PROSITE; PS00254; INTERLEUKING.

DR SWART; SM00126; IL6; 1.

DR ROSITE; PS00254; INTERLEUKIN 6; 1.

RWA Acute phase; Cytokine; Glycoprofein; Growth factor; Signal.

TICNAL 1 29 By similarity.

TICNAL 30 212 Interleukin-6.

TY P By similarity.

By similarity.

N-linked (GlCNAC. .) (Potential).

THINE (GlCNAC. .) (Potential).
                                                                                                                                                                                                                                                                                                                              Infollution piles 1953 (1995).

J. Immunol. 155.3946 (3954 (1995).

-!- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into 19-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LIORLINWMLWVIDECFRDLCYRT
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                                                                                                                                                                       Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                              Chikkala N., Ansari A.A.;
                                                                                                                                                                                                                                                                                            Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A. "Comparative sequence analysis of cytokine genes from human and
                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                              212 AA
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                                                                                                                                                                                                                                                                                MEDLINE=96003435; PubMed=7561102;
                                                                                                                                               Interleukin-6 precursor (IL-6).
:| :::| ::| 194 ILRSFKEFLQCSLRAL 209
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HSSP; P05231; 1ALU.
                                                                                                                                                                                                                 Cercopithecinae; Cercocebus
                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                        nonhuman primates."
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=FUj;
                                                                                                                                                                                                                            NCBI_TaxID=9531;
                                                                                                                                                            Name=IL6;
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IL6_CERTO
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SVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVL 177
                                                                                  136 SEEGARAVQMSTKVLIQLLQKKAKNLDAITTPEPTTNASLLTKLQAQNQWLQDMTTHLIL 195
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MEDLINE=87053818; PubMed=3023045;
Zilberstein A., Ruggieri R., Korn J.H., Revel M.;
"Structure and expression of cDNA and genes for human interferon-beta-
2, a distinct species inducible by growth-stimulatory cytokines.";
EMBO J. 5:2529-2537(1986).
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May L.T., Helfgott D.C., Sehgal P.B.;
"Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mNNA in tumor necrosis factor-treated human fibroblasts:
structural studies of the beta 2 interferon involved.";
Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P05231; Q9UCU2; Q9UCU3; Q9UCU4;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-2004 (Rel. 45, Last annotation update)
Interleukin-6 precursor (IL-6) (B-cell stimulatory factor 2) (BSF-2) (Interferon beta-2) (Hybridoma growth factor) (CTL differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89391958; PubMed-2789513; Tonouchi N., Maw K., Karaeuyama H., Matsui H.; Mwa K., Karaeuyama H., Muaran B. V., Maraeuyama H., Muman BSF-2 mRNA causes stabilization of 1 untranslated region of human BSF-2 mRNA causes stabilization of the mRNA and high-level expression in mouse NIH3T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning and expression of hybridoma growth factor in
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Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 AA
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MEDLINE=87065033; PubMed=3491322;
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MEDLINE=88082664; Pubmed=3500852;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-22388257, PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE-22388257, PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., D. Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., M. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Makealey R.W., Touchman J.W., Green B.D., Dickson M.C., Marke R.M., Blakealey R.W., Krzywinski M.I., Skalska U., Smailus D.E., M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90121567; PubMed=2610854;
Ming J.E., Cernetti C., Steinman R.M., Granelli-Piperno A.;
"Interlukin 6 is the principal cytolytic T lymphocyte differentiation
factor for thymocytes in human leukocyte conditioned medium.";
J. Mol. Cell. Immunol. 4:203-211(1989).
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                                                                                                                                                          MEDLINE-89193317; PubMed-3266463;
Wong G., Witek-Giannotti J., Hewick R., Clark S., Ogawa M.;
"Interleukin 6: identification as a hematopoietic colony-stimulating
                                                                                     "Structural analysis of the sequence coding for an inducible 26-kDa
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SEQUENCE OF 30-40, AND GLYCOSYLATION.
MEDLINE=91355644; PubMed=1883960; DOI=10.1016/1043-4666(91)90018-9;
                                                                                                                                                                                                                                                                                                                                                                      C.L., Yi
                                                                                                                                                                                                                                                                                                                                                                                                "SeattleSNPs. NHLBI HL66682 program for genomic applications, UM-
FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
                                                        Haegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                   Behring Inst. Mitt. 83:40-47(1988)
                                         MEDLINE=87004683; PubMed=3758081;
                                                                                                                                                                                                                                                                 MEDLINE=93178270; PubMed=1291290;
                                                                                                   protein in human fibroblasts."
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                                                                                                                                              SEQUENCE FROM N.A.
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                           IISSUE=Fibroblast;
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                                                                                                                                                                                                                                   Breton J., la Flura A., Bertolero F., Orsini G., Valsasina B., Zilicto R., de Filippis V., Polverino de Laureto P., Fontana A.; "Structure, stability and blological properties of a N-terminally truncated form of recombinant human interleukin-6 containing a single
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Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
"Folding topologies of human interleukin-6 and its mutants as studied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89286115; PubMed-2472117;
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"Disulfide structures of human interleukin-6 are similar to those of
human granulocyte colony stimulating factor.";
Arch. Biochem. Biophys. 272:144-151(1989).
                                                                                                                                                                      SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING FIRST DISULFIDE BOND.
MEDLINE=95154344; PubMed=7851440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E., Cumming D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97303053; PubMed=9159484; DOI=10.1006/jmbi.1997.0933;
day L.T., Shaw J.E., Khanna A.K., Zabriskie J.B., Sehgal P.
Marked cell-type-specific differences in glycosylation of
interleukin-6...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Solution structure of recombinant human interleukin-6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                    disulfide bond.";
Eur. J. Biochem. 227:573-581(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Mol. Biol. 268:468-481(1997).
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Biochemistry 35:273-281(1996).
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                                                                                                 Cytokine 3:204-211(1991).
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Gapa

14;

92; Indels

38; Mismatches

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                                                                 58 GICKGILEPAAIPHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGK 117
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                                                                                                         16 LGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2; Hernandez B.C., Suarez C.F., Mendez J.A., Echeverry S.J., Murillo L.A., Patarroyo M.E.; Midentification, Coning, and sequencing of different cytokine genes in four species of owl monkey."; Immunogenetics 54:645-653(2002). EMBL; AF097323; AAF21298.1; -...
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO: 0005525; C: extracellular; IEA.

R GO; GO: 0005125; F: cytokine activity; IEA.

R GO; GO: 0005125; F: cytokine activity; IEA.

R GO; GO: 0005138; F: interleukin-6 receptor binding; IEA.

R InterPro; IPR00357; Fimmune response; IEA.

R InterPro; IPR003573; IIé MGF GCSF.

R InterPro; IPR003573; IIé MGF GCSF.

R PRINTS; PR00493; ILG; 1.

R PRINTS; PR00493; ILG; 1.

R PRINTS; PR00493; INTERLEUKING.

R PRINTS; PR00493; INTERLEUKING.

R PROMIFS; PR00436; INTERLEUKING.

R PROMIFS; INTERLEUKING.

R PROMITER; PS00254; INTERLEUKING.

R PROMITER; PS00254; INTERLEUKING; 1.
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196 RSFKEFLQSSLRAL 209
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RESULT

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Interpro; IPR0015,",

R Pfam; PR00489; IL6; 1.

DR PRINTS; PR00434; INTERLEUKING.

DR PRODOM; PR004356; Interleukin_6; 1.

DR PROSTE; PR00554; INTERLEUKING.; 1.

THE SHORT SHOW STATE SH
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-!- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, hepatocytes it induces acute phase reactants (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-6 superfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and
                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Interleukin-6 precursor (IL-6).
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IL6 MACMU
                                                                                                                                                                                                                                                                                                                                                              Name=IL6;
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209
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SEQUENCE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu S., Meng M., Gao R.;

"Cloning and expression of interleukin 6 gene from Landrance x Meishan hybrid swine.";

"Cloning and expression of interleukin 6 gene from Landrance x Meishan Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: IL-6 is a cytckine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into IG-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91338547; PubMed-1873476; DOI=10.1016/1043-4666(91)90494-X; Richards C., Sakharvala J.; Molecular cloning and sequence of porcine interleukin 6 cDNA and expression of mRNA in synovial fibroblasts in vitro.";
                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERMY PRO0489; IL6; 1.
PRINTS; PRO0433; IL6GCSFMGF.
PRINTS; PRO0434; INTERLEUKING.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
30 212 Interleukin-6.
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                                                                                                                                                                                                          01-AUG-1992 (Rel. 23, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-6 precursor (IL-6).
                                                                                                                                                                    212 AA
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InterPro; IPR003079; 4 helix cytokine.
InterPro; IPR003573; IL6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Reprod. Dev. 32:324-330(1992)
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EMBL; M80258; AAC27127.1; -.
EMBL; AF309651; AAC27730.1; -.
PIR; 146590; 146590.
PIR; 146621; 146621.
                        : | : :: | : 1 | 194 ILRSPKEFLQSNLRAL 209
176 VLSAMEKFAGQAVRVL 191
                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
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                                                                                                                                                               IL6 PIG
P26893; Q95KN6;
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76 EKCENSKEVLAENNIALPKWAEKDGCFQSGFNQETCLMRITTGLVEFQIYLDYLQKEYES 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 GICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 SVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 KHIRYILDGISALRKETCNKSNMCESSKEALAENNINLDKMAEKDGCFQSGFNEETCLVK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| | | | | | : :: | ::: | ::: | ::: | ::: | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 1.1. | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 VGSLLVSGTRGKLPDAPEFE-------KDLLIQRLNWMLWVIDECFRDLCYRT
                                                                                                                                                                                                                                                                                                                                                                          17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification, cloning, and sequencing of different cytokine genes in four species of owl monkey."; Immunogenetics 54:645-653(2002).
EMBL; AF014510; AAD01536.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Aotinae, Aotus.
NCBI_TaxID=37293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22354194; PubMed=12466897; DOI=10.1007/800251-002-0512-2; Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J., Murillo L.A., Patarroyo M.E.;
                                                                                                                                                                                                                                                                  DB 1; Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 209;
                                                                                                                                                                                                                                                                                                                                                                          Indels
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By similarity.
By similarity.
E -> G (in Ref. 1).
; 1E736FB230B4FC5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOS, GO: 0005576; C:extracellular; IEA.
GO; GO: 0005516; F:eytokine activity; IEA.
GO; GO: 0005518; F:interleukin-6 receptor binding; IEA.
GO; GO: 000555; P:immune response; IEA.
InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR005573; IL6 MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 AA; 23406 MW; E84F085DD84002DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 16:3%; Score 179; DB 2; 1 Similarity 26:5%; Pred. No. 2.9e-08; 41; Conservative 34; Mismatches 80;
                                                                                                                                                                                                                                                            ch 16.5%; Score 180.5; DB 3 Similarity 23.9%; Pred. No. 2.1e-08, 47; Conservative 46; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aotus nancymaae (Ma's night monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0433; ILGGCSFMGF.
PRINTS; PRO0434; INTERLEUKING.
PRODOM; PD004356; Interleukin_6; 1.
SWART; SM00126; ILG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00254; INTERLEUKIN_6; 1.
72 78 BY
101 111 BY
30 30 E.
212 AA; 23952 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 SAME---KFAGQAVRVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ::| :|: :|::
| 196 RSLEDFLQFSLRAIRIM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin-6 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lai A.C.K.;

"Cloning and expression of equine interleukin-6.";

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: IL-6 is a cytckine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 IGLILVMATAFPTPLPLGEDETTSNGPLLTTADKTKQHIKYILGKISALKNEMCNNFSKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 VGSLLVSGTRGKLP----DAPEFEKDLLI-----QRLNWMLWVIDECFRDLCYRTGIC
                                                                                                                                                                                                                            MEDINE=20579380; PubMed=11137120; DOI=10.1016/S0165-2427(00)00241-5; Swiderski C.E., Sobol G., Lunn D.P., Horohov D.W.; "Molecular cloning, sequencing, and expression of equine interleukin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
"Molecular cloning of equine interleukin-6.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
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By similarity.
By similarity.
N-linked (GlCNAC. ..) (Potential).
N-linked (GLNAC. ..) (Potential).
IS -> FF (in Ref. 1).
T -> A (in Ref. 3).
                                       Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 208;
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PRINTS; PR00434; INTERLEUKING.
PRODOM; PD004356; Interleukin_6; 1.
SMART; SM00126; I.E.; 1.
PROSTIE; PS00224; INTERLEUKIN 6; 1.
Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A62F4C234056BF66 CRC64;
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I -> V (in Ref. 2)
V -> I (in Ref. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%; Score 173.5; DB 1
26.0%; Pred. No. 9.1e-08;
ive 37; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                          Vet. Immunol. Immunopathol. 77:213-220(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P05231; IALU.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; IL6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF005227; AAB62246.1; -.
EMBL; AF041975; AAC04574.1; -.
PIR; T09216; T09216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23325 MW;
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8
137
205
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caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 2
208 AA;
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                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                          NCBI_TaxID=9796;
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                                       97 LADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRG 156
                                                                                          :: | | | | | | :: | | | :: | | | :: | | | :: | | | : | | | :: | | | :: | | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Lee D., Yoo H., Choi I.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AFS18322, AAM74938.1; -.
HSSP; P05231; 1ALU.
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SMART; SM0126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
SEQUENCE 212 AA; 23881 WW; 1F540E7030BCFD77 CRC64;
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GO; GO:000518; F:cytokine activity; IEA.
GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IRR003979; 4 Helix cytokine.
InterPro; IPR003573; IL6 WGF GCSF.
InterPro; IPR003574; Interleukin_6.
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Mammalia, Butheria, Cetartiodactyla, Suina, Suidae,
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Last annotation update)
                                                                                                                                                                                                                                                                       175 LLTKLÓAQNQWLQDMTTHLILRSFKEFLQSSLRAL 209
                                                                                                                                                                                             157 LLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVL 191
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192 ILILRSLEDFLQFSLRAIRIM 212
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Interleukin-6 precursor (IL-6)
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PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKING.
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BISKEVLAENNLANLPKWAEKDGCFQSGFNQETCLAKITTGLSEFQIYLAYLQNEFKGEKE 135
                                   121 NVDVMELLIKTLGWDIQEELNKLIKTHYS--PPKFDRGLLGRLQGLKYWVRHFASFYVLS 178
                                                   Soc. Exp. Biol. Med. 204:301-305(1993).
FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of Buctions it plays an essential role in the final differentiation plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Lymphocytes;

Bradley 94062249; PubMed=8234373;

Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;

"Molecular cloning and characterization of a cDNA encoding feline
                                                                                                                                                                                                                                                     Pelis silvestris catus (Cat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=94162386; PubMed=8117820;
Ohashi T., Matsumoto Y., Watari T., Goitsuka R., Tsujimoto H.,
Hasegawa A.;
"Molecular cloning of feline interleukin-6 cDNA.";
J. Vet. Med. Sci. 55:941-944(1993).
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                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-6 precursor (IL-6).
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By similarity.
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InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; IL6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; IL6; 1.
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PRINTS; PRO0434; INTERLEUKING.
PRODOM; PD004356; Interleukin_6; 1.
SMART; SM00126; ILG; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                      PRT;
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                                                                                                                                                                     STANDARD;
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208
74
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P41683;
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               T -> N (in Ref. 2).
S -> P (in Ref. 2).
E -> K (in Ref. 2).
AKLOSOEMLRHTTI -> LSCSHRRVAEAHNN (in Ref. 2).
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Lama glama (Llama).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Cetartiodactyla, Tylopoda, Camelidae, Lama.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Raadan O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C.,
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                                                                                                                                                                                                                     14.9%; Score 163.5; DB 1; Length 208; 26.8%; Pred. No. 7.5e-07;
                                                                                                                                                                                                                                                                     84; Indels
                                                                                                                                        3 -> LR (in Ref. 2).
93B4456B2989CA4C CRC64;
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29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 AA.
                                                                                                                                                                                                                                                                     39; Mismatches
  By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (or send an email to license@isb-sib.ch)
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HTTIHLTLRRLEDFLQFSLRAVRIM 208
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Interpro, IPR003573; IL6 MGF GCSF.
Interpro, IPR003574; Interleukin 6.
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                                                                                                                                               201 F7
23401 MW;
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PRINTS; PR00434; INTERLEUKING.
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107
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Best Local Similarity
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12 VGSLLVSGTRGKLP-DAPEFEKDILIQRLNWMLWVIDECFRDLCYRTGICKGILEPAAIF 70
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8
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ProDom; PD004156; Interleukin_6; 1.
SWART; SW00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
Acute phase; Cytokine; Growth factor; Signal.
SIGNAL 1 29 By similarity.
CHAIN 30 211 Interleukin-6.
DISULFID 71 77 By similarity.
DISULFID 100 110 By similarity.
SEQUENCE 211 AA; 23988 MW; BB82D263F0996B16 CRC64;
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208 VRIM 211
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Search completed: March 30, 2005, 22:05:42 Job time : 216.063 secs

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Scoring table:

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The interleukin-6 (IL-6) fragment and protein AAW23944 can be used to detect antibodies and antibodies can be used to detect IL-6. This can be used for the diagnosis of HHV8 infection or associated diseases such as Kaposi sarcoma or Kidney cell carcinoma. Antibodies, proteins and the gene sequence can all be used in the treatment of infections and diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viral interleukin-6 produced recombinantly from human herpes virus 8 DNA - and related nucleic acid and antibodies, used for diagnosis and treatment of herpes 8 infection or related diseases, e.g. Kaposi sarcoma.
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Best Local Similarity 100.0%; Score 103; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 0; Indels
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ADL89571
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ADL89587
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Fleckenstein B,
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Aau02910
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Compugen Ltd.
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                     GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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AAR60125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to mammalian cytokine interleukin-B30 (IL-B30) polypeptides. Host cells containing a vector comprising the IL-B30 mucleic acids are used for the recombinant production of the proteins.

The polymucleotides are useful for diagnosis of IL-B30 mediated conditions, and forensic science (e.g. to distinguish rodent from human, or as marker to distinguish between different cells exhibiting fiderential expression or modification patterns). The IL-B30 (including fragments), together with antibodies that bind to IL-B30 are useful for teaching purposes. They are also used for treating conditions associated with abnormal physiology or development, including inflammatory conditions. The polypeptide cytokine should mediate cytokine synthesis and proliferation in cells. IL-B30 is useful for drug screening to identify compounds having binding affinity to IL-B30. The present sequence represents a Kaposis's sarcoma herpes virus IL-6. (Updated on 27 AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Newly isolated or recombinant polynucleotide encoding mammalian cytokine interleukin-B30 (IL-B30), including fragments - useful for regulating activation, development, differentiation and function of various cell types, and for diagnosing and treating conditions associated with IL-B30.
                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation; inflammatory condition; drug screening; human; IL-6.
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iive 0; Mismatches 0;
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                                             1 GFNETSCLKKLADGFFEFE 19
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                                                                                                                                                                                                                                                                                       27-AUG-2003
21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-1999.
                                                                                                                                                                                                                                         AAW95015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bazan JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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AAW40103 standard; protein; 204 AA

AAW40103 ID AAW4

RESULT 3

1 GFNETSCLKKLADGFFEFE 19

GFNETSCLKKLADGFFEFE

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The sequence represents a novel human herpesvirus 8 (HHV-8) interleukin-

6. The invention claims for novel genes, which includes the viral

contentiatin-6 gene, found at the divergent Di-B locus HHV-8 divergent

clocus Di-B lies between open reading frames 11 and 17. Sequencing of the

HHV-8 divergent locus Di-B revealed the presence of nine viral ORFs with

CC HHV-8 divergent locus Di-B revealed the presence of nine viral ORFs with

CC HHV-8 divergent locus Di-B revealed the presence of nine viral ORFs with

CC AAW40101), Bcl-2 homologue (AAW40102), dibydrofolate reductase (DHFR, see

CC AAW40101), Bcl-2 homologue (AAW40102), dibydrofolate reductase (DHFR, see

CC AAW40101), Bcl-2 homologue (AAW40102), IE-1A (AAW40105)

CC and, four cytokines which include viral interleukin-6 (VIL-6), viral

macrophage inhibitory protein (VMIP)-1A (AAW40104) and -1B (AAW40105)

CC beta-chemokine-like (BCK, AAW40106) protein. The invention claims the

CC mentioned proteins and a polymucleotide containing HHV-8 genes encoding

CO mentioned proteins and polymucleotide containing that the

CC using antibodies to the proteins way be used directly or indirectly, e.g.

CL using antibodies and the proteins way be used directly or indirectly, e.g.

CL using antibodies containing compounds for divise to treat HHV-8

CL claimed to be useful in screening compounds for drugs to treat HHV-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human herpes virus gene region containing 8 open reading frames -
useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                     DL-B; thymidylate synthase; dihydrofolate reductase; primer; HHV-B; Bcl-2 homologue; IE-1A; IE-1B; viral macrophage inhibitory protein; Kaposi's sarcoma; beta-chemokine-like; amplification; PCR; vIL-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicholas J, Reitz MR, Hardwick JM;
                                                                                                                   Human herpesvirus 8 (HHV-8) interleukin-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 59-60; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW23944 standard; protein; 204 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US012931.
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                                         (first entry)
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Les 19; Conservative
(revised)
                                                                                                                                                                                                                                                                                                                                                          Human herpesvirus 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-130422/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9804284-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-1998
    27-AUG-2003
                                     15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW23944
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This is the amino acid sequence of the kaposi sarcoma herpes-like virus/interleukin-6, used in the method of the invention. In this method, an antiviral agent effective against Kaposi sarcoma herpes-like virus (KSHV), is used to prevent progression of MGUS to multiple myeloma or related malignancy. KHSV- and/or interleukin-6 related disorders such as specifically Alzheimer's disease, multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, scleroderma and malignancies of kidney or head/neck. The vaccines (comprising a KHSV-specific immunogen) is used to produce a therapeutic and/or prophylactic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAC3; interleukin-6; IL-6; inhibitor; IL-6-inhibitory; lymphoma; leukaemia; myeloma; carcinoma; sarcoma; chronic inflammation; bacterial; viral infection; osteolysis; degenerative disease;
                                                                                                                                                                          Treatment of multiple myeloma and monoclonal myopathy with antiviral agent - active against Kaposi sarcoma virus, or with inhibitory nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New protein PAC3, useful for treating cancers, is an inhibitor interleukin-6, also related peptides, nucleic acid, antisense oligonucleotides and transformed cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-6 inhibiting human PAC3 protein, SEQ ID No 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 103; DB 2;
100.0%; Pred. No. 1.9e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunological disorder; transgenic animal; human
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CENT BERRARD LEGON.
INSERM INST NAT SANTE & RECH MEDICALE.
HOSPICES CIVILS LYON.
                                                                                Vescio RA;
                                                                                                                                                                                                                   acid or antibody against this virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH76487 standard; protein; 118 AA.
                                                                                                                                                                                                                                                       Disclosure; Fig 5B; 137pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFNETSCLKKLADGFFEFE 105
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Matches 19; Conservative
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BERENSON J R.
RETTIG M B.
VESCIO R A.
                                                                              Berenson JR, Rettig
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                                                                                                                  WPI; 1998-480765/41.
                                                                                                                                      N-PSDB; AAV54070
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                                          (VESC/)
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    (BERE/)
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(INRM )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The interleukin-6 (IL-6) and protein AAW23945 derived from the sequence can be used to detect antibodies and antibodies can be used to detect IL-6. This can be used for the diagnosis of HHV8 infection or associated diseases such as Kaposi sarcoma or kidney cell carcinoma. Antibodies, proteins and the gene sequence can all be used in the treatment of infections and diseases as mentioned above
                                                                                                                                                                                                                                                                                                                                                                                                                            Viral interleukin-6 produced recombinantly from human herpes virus 8 DNA - and related nucleic acid and antibodies, used for diagnosis and treatment of herpes 8 infection or related diseases, e.g. Kaposi sarcoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaposi sarcoma herpes-like virus/interleukin-6; PCR; primer; antiviral agent; multiple myeloma; vaccine; rheumatoid arthritis; monochonal gammopathy of undetermined significance; MGUS; malignant; interleukin-6; Alzheimer's disease; multiple sclerosis; scleroderma; systemic lupus erythematosus; amplification.
                                      human herpesvirus 8; HHV8; shotgun-cloning;
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                                                                                                                                                                                                                                                                                                                                                   Pleckenstein B, Albrecht J, Neipel F,
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    Human herpesvirus 8 interleukin-6
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                                        interleukin-6; IL-6;
                                                          antibody; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-120781/11.
                                                                                              Human herpesvirus 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 204 AA;
                                                                                                                                    WO9803657-A1
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11-NOV-1997;
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Gaps

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Indels

Length 204;

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nucleic acid, antisense

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PAC3; interleukin-6; IL-6; inhibitor; IL-6-inhibitory; lymphoma; leukaemia; myeloma; carcinoma; sarcoma; chronic inflammation; bacterial; viral infection; osteolysis; degenerative disease; immunological disorder; transgenic animal; human.
                                                                                                                                                                                                                                                                                                                                                          Interleukin-6 inhibiting human PAC3 protein, SEQ ID No 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. (HOSP-) HOSPICES CIVILS LYON.
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(BERA-) CENT BERARD LEON.
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                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                           Sequence 118 AA;
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                                                                                                                                                                                              invention.
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                                                                                                                                                                                                                                          Matches
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and the properties of the control of the nucleic acid; antisense and codes PAC3 or the fragments of the nucleic acid; antisense coligonucleotides that block transcription or translation of PAC3 or its fragments, able to hybridize to the PAC3 coding nucleic acid; a transcenic, non-human animal that expresses a transgene for PAC3 or its fragments; an expression vector containing PAC3 coding nucleic acid and expression elements; and microorganisms or host cells transformed with the vector containing the PAC3 coding nucleic acid and expression the vector containing the PAC3 coding nucleic acid and expression clements. The PAC3 protein, and its active fragments, are used to treat lymphoma, leuksemia, myeloma, carcinoma and sarcoma, other conditions induced by, or associated with, overexpression of interleukin-6, e.g. chronic inflammation, bacterial or viral infections, osteolysis in codes PAC3 can be used for recombinant production of the protein and to prepare transgenic animals, useful as models for studying, in vivo, prepare transgenic animals, useful as models for studying, in vivo, excessive expression of the PAC3 coding nucleic acid, or its truncated or mutated forms. This sequence represents a human PAC3 protein of the
                                                                                                                                                                                                       The invention relates to a novel protein, PAC3, which inhibits interleukin-6 (IL-6) and has a 125 amino acid sequence, given in the specification. The invention further relates to: peptide fragments of PAC3 with IL-6-inhibitory activity, formed by addition, suppression and/or replacement of one or more amino acids, a nucleic acid that
interleukin-6, also related peptides, n
oligonucleotides and transformed cells.
                                                                                                                       Claim 1; SEQ ID NO 3; 39pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 125 AA;
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                                                                                                                   The invention relates to a novel protein, PAC3, which inhibits interleukin-6 (IL-6) and has a 125 amino acid sequence, given in the specification. The invention further relates to: peptide fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 0.076;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                       Claim 3; SEQ ID NO 4; 39pp; French
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                                                                                                                                                                                                                                                                                                        Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor IC; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                 Gaps
                                                                                                                                                                                                                                                                                Angiotensin converting enzyme (ACEV) splice variant protein #10.
                                 ;
0
59.2%; Score 61; DB 7; Length 125; 57.9%; Pred. No. 0.08; ive 2; Mismatches 6; Indels
                                                                                                                                                                                AAU02910 standard; protein; 148 AA.
                                                                  1 GENETSCLKKLADGFFEFE 19
                                                                                    11 GFNEETCLVKIITGLLEFE 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99IL-00133455.
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                                                                                                                                                                                                                                                (first entry)
                Local Similarity 57.9 ses 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200136632-A2
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                                                                                                                                                                                                                AAU02910;
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(COMP-) COMPUGEN LTD

New protein PAC3, useful for treating cancers, is an inhibitor of

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The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acidis are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various candidate compounds castaler diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                              Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.2%; Score 61; DB 4; Length 148; 57.9%; Pred. No. 0.095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                       Bernstein J;
                       Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                         Claim 4; Fig 10; 519pp; English.
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                       Azar I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 57.5
Les 11; Conservative
                                                               WPI; 2001-336004/35.
N-PSDB; AAS06010.
                  David A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 148 AA;
                       Levine Z,
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59 41 GFNEETCLVKIITGLLEFE 셤

ADF17513 standard; protein; 157 (first entry) MB-2 amino acid sequence WO2003091720-A1. 12-FEB-2004 Synthetic. ADP17513; RESULT 9 ADF17513 ID ADF1

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protein structure analysis; genetic analysis.

06-NOV-2003.

25-APR-2003; 2003WO-JP005344.

26-APR-2002; 2002JP-00127399.

AJINOMOTO CO INC. UMEYAMA H. (AJIN) (UMEY/) Hirayama K; Suzuki E, Umeyama H, Yamada N,

4PI; 2003-877362/81.

Protein structure analysis comprising measuring a fragmented spectrum, determining classification information, determining information about an easily cut off region, estimating the stereostructure of the protein and outputting results.

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The present invention describes a protein structure analysis method comprising measuring a fragmented spectrum by dividing the target protein into several segments, determining the classification information of the segmented ion corresponding to the amino acid sequence based on the segmented ion corresponding to the amino acid sequence based on the segmented location, estimating the stereo classification based on the segmented location, estimation data and structure of the protein, and outputting result of estimation data and easy cut off region information. Also described: (1) a similar method wherein before estimating the stereo structure, residual solvent information; (2) a similar method wherein a composite of a protein and a compound is fragmented, and before estimating the stereo structure the information of mutual effect of the protein and /or compound is compound of mutual effect of the protein and /or compound is determined; (3) apparatus for carrying out the above methods; and (4) programs for carrying out the methods can be used for genetic analysis. The present sequence represents an MB-2 amino acid sequence, which is used in an example from the present invention.
                           3xample 5; Fig 18; 103pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 157 AA;
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59.2%; Score 61; DB 7; Length 157; 57.9%; Pred. No. 0.1; ive 2; Mismatches 6; Indels 89 1 GFNETSCLKKLADGFFEFE 19 GFNEETCLVKIITGLLEFE Best Local Similarity 57.9 Matches 11; Conservative Query Match 셤 ઠ

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Gaps ö

RESULT 10

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Gaps

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AAR77391 standard; protein; 162 AA.

AAR77391;

17-APR-1996 (first entry)

Human mutant IL-6a'Cl (amino acids 5-19 and 44-50 deleted).

Human interleukin-6; IL-6a'C1 mutant; increased stability; recombinant; production; deletion mutant; amino acids 5-19 and 44-50.

Homo sapiens

JP07224097-A

22-AUG-1995

08-FEB-1994;

94JP-00014461. 08-FEB-1994;

(ASAG) ASAHI GLASS CO LTD

WPI; 1995-325556/42.

N-PSDB; AAQ94346

Interleukin-6 mutant, related DNA and expression vectors - has higher stability than natural interleukin-6.

Claim 1; Page 14; 18pp; Japanese.

AAQ94346 encodes AAR77391 the human IL-6 deletion mutant IL-6a'Cl, which lacks the amino acids G195-Leu19 and Cys44-Cys50 of the wild type protein. The CDNA can be used for the recominant prodn. of IL-6a'Cl, which has increased stability compared to wild type IL-6

Sequence 162 AA

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Local Similarity
                                                                                                                                                                                                                                                                                                                                      Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003068300-A1.
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                                                                  Homo sapiens
                                                                                                                       01-FEB-1996;
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Matches
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ABU62834
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                                                                                                                                                                                                                                                                                                                                                                                                                                    A multicloning vector, comprising the human interleukin-6 (hIL-6) cDNA, Schizosaccharomyces pombe secretory signal peptide fragment or P-factor fragment (PO fragment) DNA and preferably an animal cell viral promoter sequence and a neomycin resistance gene, can be used for the efficient production of a hIL-6 fragment, i.e. the present sequence, in a fission yeast host, preferably 8. pombe, culture
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe secretory signal peptide (P-factor) gene - production of vectors for expression of animal proteins in a fission yeast, pref. S. pombe, host.
                                                                                                                                                                                    Secretory; signal peptide; P-factor; multicloning vector; PCR; animal protein; expression; production; recombinant; primer; fission yeast; human; serum albumin; interleukin-6; polymerase chain reaction; Schizosaccharomyces pombe; PO fragment.
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          Length 162,
                            6; Indels
                                                                                                                                                                                                                                                                                                                                               Kumagai H;
          Score 61; DB 2;
Pred. No. 0.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.1;
2; Mismatches
                           2; Mismatches
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                                                                                                                                                                                                                                                                                                                                               Tsukamoto H,
                                                                                                            AAW00131 standard; protein; 162
                                               GFNETSCLKKLADGFFEFE 19
                                                         GFNEETCLVKIITGLLEFE 73
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          59.2%;
                                                                                                                                                                   Human interleukin-6 fragment.
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GFNEETCLVKIITGLLEFE
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Query Match
Best Local Similarity 57.5%,
--hes 11; Conservative
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                                                                                                                                                                                                                                                                                                                                              Tohda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 162 AA;
                                                                                                                                                 09-APR-1997
                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                   WO9623890-A1
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Matches
                                                                                            RESULT 11
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ID AAW
XX AC AAW
XX DT 09-3
XX DE Hum
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Human, interleukin-6; IL-6; cytokine; bone homeostasis; Paget's; disease; multiple myeloma; post-menopausal bone loss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A multicloning vector, comprising the human interleukin-6 (hIL-6) cDNA, Schizosaccharomyces pombe secretory signal peptide fragment or P-factor fragment (P1 fragment) DNA and preferably an animal cell viral promoter sequence and a neomycin resistence gene, can be used for the efficient production of a hIL-6 fragment, i.e. the present sequence, in a fission yeast host, preferably S. pombe, culture
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Secretory; signal peptide; P-factor; multicloning vector; PCR; animal protein; expression; production; recombinant; primer; fission yeast; human, earum albumin; interleukin-6; polymerase chain reaction; Schizosaccharomyces pombe; P1 fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kumagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nikaido K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 7; Page 30-31; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU62834 standard; protein; 166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tohda H, Tsukamoto H,
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29-APR-1997; 97US-00841035.
07-FEB-2000; 2000US-00499148.
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                                                                                                                                                                                                                                                                                                                                                                                     96WO-JP000198,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASAG ) ASAHI GLASS CO LTD
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The invention relates to a computer system comprising computer hardware and model of interleukin (IL)-6 structure, where the model has data set representing phasing statistics for the native crystal, root mean square (RMS) deviations from experimental distance restraints (Angstrom), RMS deviations from idealised covalent geometry, energetics, interhelical and kink angles and interhelical distances, residues conserved among 9 species of IL-6, as given in specification. Also included are identifying a species which is an agonist or antagonist of IL-6 activity or binding using the computer system, an agonist or antagonist species identified by above mentioned method and identifying a substance that inhibits or mimics IL-6 activity or binding, using the computer system. Il-6 is a cytokine involved in bone homeostasis. Increased levels of IL-6 have been correlated with Paget's disease and multiple myeloma. IL-6 is a lso
                                                                                   Computer system useful for identifying agonist or antagonist of interleukin 6 activity or binding, comprises computer hardware and model of interleukin 6 structure.
    Hong
    Yu H,
    Mcdonagh TE,
    Xu G,
  Seehra JS,
                                                                                                                                                                                    Disclosure; Fig 12; 37pp; English.
  Stahl ML,
                                             WPI; 2003-540877/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 166 AA;
  Somers WS,
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59.2%; Score 61; DB 6; Length 166; 57.9%; Pred. No. 0.11; 5; Conservative Local Similarity ses 11; Conser Query Match Matches ሯ

ABU62837 standard; protein; 166 AA Monkey interleukin-6, IL-6, (first entry) 16-SEP-2003 ABU62837; RESULT 14 ABU62837

Interleukin-6; IL-6; cytokine; bone homeostasis; Paget's; disease; multiple myeloma; post-menopausal bone loss; monkey.

Macaca mulatta

US2003068300-A1.

10-APR-2003.

19-SEP-2002; 2002US-00246946

96US-0024115P. 97US-00841035. 2000US-00499148. 16-AUG-1996; 29-APR-1997; 07-FEB-2000;

(AMHP) WYETH

Hong J; Yu H, Mcdonagh TE, χn g, Seehra JS, Somers WS, Stahl ML, WPI; 2003-540877/51 Computer system useful for identifying agonist or antagonist of interleukin 6 activity or binding, comprises computer hardware and model of interleukin 6 structure.

Disclosure, Fig 12; 37pp; English

The invention relates to a computer system comprising computer hardware and model of interleukin (IL)-6 structure, where the model has data set representing phasing statistics for the native crystal, root mean square (RMS) deviations from experimental distance restraints (Angstrom), RMS deviations from idealised covalent geometry, energetics, interhelical and kink angles and interhelical distances, residues conserved among 9 species of IL-6, as given in specification. Also included are identifying a species which is an agonist or antagonist of IL-6 activity or binding using the computer system, an agonist or antagonist species identified by above mentioned method and identifying a substance that inhibits or mimics IL-6 activity or binding, using the computer system. Il-6 is a cytokine involved in bone homeostasis. Increased levels of IL-6 have been to correlated with Paget's disease and multiple myeloma. IL-6 is also thought to be involved in post-menopausal bone loss. The present sequence is an IL-6 protein from a species other than human, used in the

Sequence 166 AA;

Gaps ö Length 166; 6; Indels DB 6; Score 61; DB 6; Pred. No. 0.11; 2; Mismatches 59.2%; 11; Conservative 3est Local Similarity Query Match Matches

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1 GFNETSCLKKLADGFFEFE 19 |||| :|| |: | ||| GFNEDTCLVKIITGLLEFE 77 ठ

ADC20004 standard; protein; 166 AA ADC20004; RESULT 15

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Gaps

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6; Indels

Mismatches

rhesus monkey; crystal; interleukin-6; IL-6; Rhesus monkey interleukin-6, IL-6. 18-DEC-2003 (first entry)

Macaca mulatta.

IL-6/IL-6 receptor interaction.

US6461604-B1. 08-OCT-2002

96US-0024115P 97US-00841035 07-FEB-2000; 2000US-00499148 16-AUG-1996; 29-APR-1997;

(GEMY) GENETICS INST LLC.

۵, Hong Yu H, Mcdonagh TE, Xu G, Seehra JS, Stahl ML, WPI; 2003-719565/68. Somers WS,

Crystalline human interleukin-6, useful for identifying IL-6/IL-6 receptor interactions, and for identifying agonists and antagonists of such interactions, has diffracting crystals of a specific space group.

Disclosure, SEQ ID NO 4; 30pp; English

The invention relates to crystalline human interleukin-6 (IL-6). The crystalline form of IL-6 is useful for identifying IL-6/IL-6 receptor interactions, and for identifying agonists and antagonists of the interactions. Crystalline IL-6 structure enables effective study of its interactions with its receptor. The present sequence represents the amino acid sequence of rhesus monkey interleukin-6, IL-6.

Sequence 166 AA;

0; 0; Gaps Query Match 59.2%; Score 61; DB 7; Length 166; Best Local Similarity 57.9%; Pred. No. 0.11; Matches 11; Conservative 2; Mismatches 6; Indels

1 GFNETSCLKKLADGFFEFE 19 ||||| :|| || ||| 59 GFNEDTCLVKIITGLLEFE 77

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Search completed: March 30, 2005, 22:01:42 Job time: 22.0448 secs

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68 GFNETSCLKKLADGFFEFE
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

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(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-58-089-16
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US-09-230-371A-25
US-09-230-371A-26
US-09-687-637B-37
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US-09-184-1317-10
US-08-716-317-15
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APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DANK Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: 404-1104
COMPUTER: Babala FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Bab Compatible
COMPUTER: SA-JUL-1997
ATTORNEY/AGENT INFORMATION:
TELEFRANCE CHARACTERISTICS:
TELEFRANCE CHARACTERISTICS:
SEQUENCE: Amenion acids
TELENGTH: 185 amino acids
TELENGTH: Bab Compatible
CLENGTH: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 103; DB 3; Length 185;
Pred. No. 3.4e-09;
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                                                              US-08-149-101A-17
US-08-149-101A-22
US-09-559-950A-1
PCT-US94-12873-17
PCT-US94-12873-22
5186931-1
                                                                                                                                                                                                                     US-07-918-181A-4
US-07-918-181A-6
US-07-918-181A-8
US-08-231-575-2
US-08-231-575-4
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US-07-918-181A-2
                                                   -08-945-529-12
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                                                                                                                                                                         5186931-1
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Patent No. 6060284
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
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98

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Sequence 16, Application US/09558474
Sequence 16, Application US/09558474
Patent No. 6835825
GENERAL INFORMATION:
APPLICANT: BAZAN, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304-1104

COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
    CURRENTION DATA:
    APPLICATION NUMBER: US/09/558,474
    FILING DATE: 25-Apr-2000
    CLASSIFICATION: <underween
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 103; DB 4;
100.0%; Pred. No. 3.4e-09;
tive 0; Mismatches 0;
                                                             APPLICATION DAMER: US/09/558,087
FILING DATE: 25-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION: «Unknown»
PRIOR APPLICATION OWNER: US 60/053,765
FILING DATE: 25-UL-1997
ATTORNEY, AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
TELECOMMUNICATION:
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APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-UUL-1997
ATTORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
TELECOMUNICATION INFORMATION:
TELECOMUNICATION:
TELECOMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 185 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                      Sequence 16, Application US/09558089
Patent No. 6479634
GENERAL INFORMATION
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: 1
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
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                                                                                                                                                                                                                                                                                                        SIREBLI SUL CALLILOLING AVENUES
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/558,089
FILING DATE: 25-Apr-2000
CLASSIFICATION: <underwedtedth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-089-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/122,443
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 185 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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STATE: California
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Best Local Similarity
                                                                       US-09-558-089-16
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        US-09-230-371A-26
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APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Belman, Isladore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USSS THEREOF
FILE REPERBUCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/09230637

Patent No. 6264958

JERRRAL INFORMATION:
APPLICANT: Hayward, Gary
APPLICANT: Hayward, Gary
APPLICANT: Hardward, John
JAPPLICANT: Hardward, John
JITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
JITLE OF INVENTION: Associated Herpesvirus
FILE REFERENCE: 1107.78372
CURRENT APPLICATION NUMBER: US/09/230,637
CURRENT PLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 60/022,591
PRIOR APPLICATION NUMBER: PCT US 97/12931
PRIOR APPLICATION NUMBER: PCT US 97/12931
PRIOR PILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FREEE PREEE FREEE                                                                                                                                                                                                                                     Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 204;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels

    TYPE: PRT
    ORGANISM: Kaposi's sarcoma-associated herpes-like virus
US-09-230-637-25

                                                                                                                                                                                                                    / Match 100.0%; Score 103; DB 4; Local Similarity 100.0%; Pred. No. 3.4e-09; nes 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 103; DB 3;
100.0%; Pred. No. 3.8e-09;
tive 0; Mismatches 0;
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                                    ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-474-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: PCT/US97/13346
1997-07-22
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-09-230-371A-26
; Sequence 26, Application US/09230371A
; Patent No. 6348586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-09-230-637-25
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LENGTH: 204
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Matches
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                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hirata, Yuichi
APPLICANT: Hirata, Yuichi
TITLE OF INVENTION: CTYOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIPERATION
FILE REFERENCE: 06501-067001
CURRENT APPLICATION NUMBER: US/09/687,637B
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: PCT/JP99/01997
PRIOR APPLICATION NUMBER: PCT/JP99/01997
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 46
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hirate, Yuichi
TITLE OF INVENTION: CYTOKINB-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
FILE REFERENCE: 06501-067001
CURRENT APPLICATION NUMBER: U9(09/687,637B
CURRENT FILING DATE: 2000-10-13
PRIOR PILING DATE: 1999-04-14
PRIOR PLILING DATE: 1999-04-14
PRIOR PILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 89
                                                      Gaps
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    Length 204;
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Pred. No. 0.011;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.2%; Score 61; DB 4; Length 89; 57.9%; Pred. No. 0.011; ive 2; Mismatches 6; Indels
                                                    IndelB
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                Sequence 36, Application US/09687637B Patent No. 6610285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37, Application US/09687637B Patent No. 6610285 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Cercocebus torquatus atys
                                                                                                                          87 GFNETSCLKKLADGFFEFE 105
                                                                                                 1 GFNETSCLKKLADGFFEFE 19
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Best Local Similarity 57.9%;
Matches 11; Conservative
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Macaca mulatta
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LENGTH: 163 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                        162 amino acids
  TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703-413-2220
                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein US-08-716-317-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-716-317-15
                                                                                                                  single
                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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US-08-716-317-15
                                                                        LENGTH:
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                                                                                    GENERAL INFORMATION:
APPLICANT: Hirata, Yuichi
TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
TITLE OF INVENTION: 0501-067001
CURRENT APPLICATION NUMBER: US/09/687,637B
CURRENT APPLICATION NUMBER: PCT/JP99/01997
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 5919554

GENERAL INPORMATION:

APPLICANT: HAMA, YUKKO

APPLICANT: TSUKAMOTO, HIROKO

APPLICANT: TSUKAMOTO, HIROKO

APPLICANT: KUNAGIA, HIROKO

APPLICANT: KUNAGIA, HIROKO

TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION

TITLE OF INVENTION: VECTOR CONTAINING IT

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 61; DB 4; Length 89;
Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,317
FILING DATE: 02-0CT-1996
CLASSIFICATION BATA:
APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CT/JP96/00198
FILING DATE: 01-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 17/16/1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAMME: OBLOW, NORVAN F.
REGISTRATION INFORMATION:
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 59-924-0 PCT
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
RESULT 9
US-09-687-637B-38
Sequence 38, Application US/09687637B
; Patent No. 6610285
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Best Local Similarity 57.9%;
Matches 11; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-09-687-637B-38
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US-08-716-317-10
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ORGANISM: Macaca mulatta
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                      US-09-499-148-1
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US-09-499-148-4
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                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: GARVIN, Robert T.
APPLICANT: GARVIN, Robert T.
APPLICANT: MALEK, LAWTENCE T.
TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHA
TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER H
TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 61, DB 1; Length 164;
Pred. No. 0.022;
2; Mismatches 6; Indels
 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22313-0299
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/224,568
APPLICATION NUMBER: US 07/224,568
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 18740/116 CACO
TELECOMMUNICATION INFORMATION:
TRIEDHONE: (703)836-9300
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,314
                                                                                                                                                                    Sequence 60, Application US/08318193
Patent No. 5641663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09499148
Patent No. 6461604
GENERAL INFORMATION:
                                                       56 GFNEETCLVKIITGLLEFE 74
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                                   1 GFNETSCLKKLADGFFEFE 19
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APPLICANT: STAHL, MARK L.
APPLICANT: SEEHRA, JASSIR S.
APPLICANT: XU, GUANG-YI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 164 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.9°
Matches 11; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-193-60
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                 RESULT 12
US-08-318-193-60
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Matches
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TITLE OF INVENTIONS, JIN
TITLE OF INVENTIONS: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
FILE REFERENCE: 50657-05278USC1
CURRENT APPLICATION WUMBER: US/09/499,148
CURRENT FILING DATE: 1997-4-28 AND 1996-8-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 166
TYPE: DATE
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CURRENT APPLICATION NUMBER: US/09/499,148
CURRENT FILING DATE: 2000-02-07
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SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 166
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Patent No. 5641657
GENERAL INFORMATION:
APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Interleukin-6 Splice Variant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61; DB 4;
Pred. No. 0.022;
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Patent No. 6461604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: SOMERS, WILLIAM
APPLICANT: STAHL, MARK L.
APPLICANT: SEEHRA, JASSHR S.
APPLICANT: XU, GUANG-YI
APPLICANT: MCCONAGH, THOWAS E.
APPLICANT: HONG, JIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.2%;
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Best Local Similarity 57.91
Best Local Similarity 57.91
Conservative
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Best Local Similarity 57.9
Matches 11; Conservative
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Query Match 59.2%; Score 61; DB 1; Length 167; Best Local Similarity 57.9%; Pred. No. 0.022; Matches 11; Conservative 2; Mismatches 6; Indels
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/246,427A
FILING DATE: Submitted herewith
CLASSIFICATION: 435
FILING DATE: MAY 19, 1994
CLASSIFICATION UNMBER: 08/246,427
FILING DATE: MAY 19, 1994
CLASSIFICATION UNMBER: 36,134
FILING DATE: MAY 19, 1994
CLASSIFICATION NUMBER: 36,134
FREERROCE/DOCKET NUMBER: 325800-
TELEPHAN: 101-994-1700
TELEPHAN: 201-994-1700
TELEPHAN: 201-994-1700
TELEPHAN: 101-994-1700
TELEPHAN: 201-994-1700
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Search completed: March 30, 2005, 22:11:03 Job time : 6.02691 secs

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March 30, 2005, 21:49:40; Search time 16.1031 Seconds (without alignments) 390.664 Million cell updates/sec
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1: /cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
2: /cgn2 6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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SUMMARIES

SUMMARIES

Query

Match Length DB ID

59.2 89 14 US-10-440-066-38 Sequence 37, Appl 59.2 166 14 US-10-446-946-1 Sequence 37, Appl 59.2 166 14 US-10-446-966-38 Sequence 37, Appl 59.2 166 14 US-10-546-946-1 Sequence 1, Appl 59.2 183 16 US-10-658-834A-198 Sequence 217, Appl 59.2 183 16 US-10-658-834A-896 Sequence 217, Appl 59.2 183 16 US-10-658-834A-896 Sequence 896, Appl 59.2 183 16 US-10-658-834A-896 Sequence 897, Appl 59.2 183 16 US-10-658-834A-896 Sequence 898, Appl 59.2 183 16 US-10-658-834A-899 Sequence 899, Appl 59.2 183 16 US-10-658-834A-899 Sequence 899, Appl 59.2 183 16 US-10-658-834A-890 Sequence 899, Appl 59.2 183 16 US-10-658-834A-890 Sequence 900, Appl 59.2 183 16 US-10-658-834A-901 Sequence 901, Appl
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RESULT 2 US-10-440-066-37 ; Sequence 37, Application US/10440066

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14 61 59.2 183 16 US-10-658-834A-902 15 61 59.2 183 16 US-10-658-834A-903 18 61 59.2 183 16 US-10-658-834A-903 18 61 59.2 183 16 US-10-658-834A-903 20 61 59.2 183 16 US-10-658-834A-904 20 61 59.2 183 16 US-10-658-834A-904 21 61 59.2 183 16 US-10-658-834A-904 22 61 59.2 183 16 US-10-658-834A-914 23 61 59.2 183 16 US-10-658-834A-914 24 61 59.2 183 16 US-10-658-834A-914 25 61 59.2 183 16 US-10-658-834A-914 26 61 59.2 183 16 US-10-658-834A-914 27 61 59.2 183 16 US-10-658-834A-914 28 61 59.2 183 16 US-10-658-834A-914 29 61 59.2 183 16 US-10-658-834A-914 20 61 59.2 183 16 US-10-658-834A-914 20 61 59.2 183 16 US-10-658-834A-914 21 61 59.2 183 16 US-10-658-834A-914 22 8 61 59.2 183 16 US-10-658-834A-914 23 61 59.2 183 16 US-10-658-834A-914 24 10 15 59.2 183 16 US-10-658-834A-914 25 61 59.2 183 16 US-10-658-834A-914 26 15 59.2 183 16 US-10-658-834A-914 27 11 59.2 183 16 US-10-658-834A-914 28 61 59.2 183 16 US-10-658-834A-914 29 61 59.2 183 16 US-10-658-834A-914 20 61 59.2 183 16 US-10-658-834A-914 20 61 59.2 183 16 US-10-658-834A-914 21 61 59.2 183 16 US-10-658-834A-914 22 61 59.2 183 16 US-10-658-834A-914 23 61 59.2 183 16 US-10-658-834A-914 24 61 59.2 183 16 US-10-658-834A-914 25 61 59.2 183 16 US-10-658-834A-914 26 15 59.2 183 16 US-10-658-834A-914 27 US-10-440-066-36 28 CURRENT PREDICATION NUMBER: US/10/440.066 28 US-10-40-066-36 28 US-10-40-066-36 28 US-10-40-066-36 28 US-10-40-066-36 29 US-10-40-066-36 20 US-10-40-060-36 20 US-10-40-060
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YU, HSIANG-AI
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US-10-658-834A-198
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                                 APPLICANT: Hirata, Yuichi
FILE REPERENCE: 067010.
FILE REPERENCE: 067010.
CURRENT APPLICATION NUMBER: US/10/440,066
CURRENT PILING DATE: 2003-05-15
FRIOR APPLICATION NUMBER: US/09/687,637
PRIOR PILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: DCT/JD99/01997
PRIOR PILING DATE: 1099-04-14
PRIOR APPLICATION NUMBER: US/09/687,637
PRIOR PILING DATE: 1099-04-14
PRIOR PILING DATE: 1099-04-14
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FRAESEQ for Windows Version 4.0
LENGTH: 89
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TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
FILE REFERENCE: 06501-067001
CURRENT APPLICATION NUMBER: US/10/440,066
CURRENT APPLICATION NUMBER: US/09/687,637
PRIOR APPLICATION NUMBER: US/09/687,637
PRIOR PLING DATE: 1999-010-13
PRIOR FLING DATE: 1999-04-14
PRIOR FLING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030068300A1
GENERAL INFORMATION:
APPLICANT: SOWERS, WILLIAM
APPLICANT: STERHA, MARK L.
APPLICANT: STERHA, JASBIR S.
APPLICANT: WILLIAM
APPLICANT: WILLIAM
APPLICANT: NU GUANG-YI
APPLICANT: NU GUANG-YI
APPLICANT: MCCONAGH, THOWAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 38, Application US/10440066; Publication No. US20030180256A1; GENERAL INFORMATION:
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Publication No. US20030180256A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ch 59.2%;
1 Similarity 57.9%;
11; Conservative
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Best Local Similarity 57.9%;
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                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Macaca mulatta US-10-440-066-37
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CORGANISM: Homo sapiens
US-10-440-066-38
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Best Local Similarity
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APPLICANT: Gattier, Rene
APPLICANT: Gattier, Theerry
APPLICANT: Guyon, Thierry
APPLICANT: Outon, Thierry
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuctions INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-922
APPLICANT: HONG, JIN

TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
FILE REFERENCE: 50657-05278USD1
CURRENT APPLICATION NUMBER: US,10/246,946
CURRENT FILING DATE: 2002-09-19
PRIOR PILING DATE: 2000-2-7, 1997-4-28 AND 1996-8-16
PRIOR FILING DATE: 2000-2-7, 1997-4-28 AND 1996-8-16
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
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TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
FILER REPERENCE: S0657-05279USDI
CURRENT APPLICATION NUMBER: US/10/246,946
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 09/499,148, 08/841,035 AND 60/024,115
PRIOR FILING DATE: 2000-2-7, 1997-4-28 AND 1996-8-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
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57.9%; Pred. No. 0.041;
tive 2; Mismatches 6; Indels
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Publication No. US20030068300A1
GENERAL INFORMATION:
APPLICANT: SOMERS, WILLIAM
APPLICANT: STAHL, WARK L.
APPLICANT: SEEHRA, UASBIR S.
APPLICANT: YOU'NG'NG'YI
APPLICANT: YU' GURNG-YI
APPLICANT: YU' HSIANG-YI
APPLICANT: YU' HSIANG-XI
APPLICANT: HONG, JIN
APPLICANT: HONG, JIN
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ORGANISM: Macaca mulatta
                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Matches 11; Conserv
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TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu-
TITLE OF INVENTION: Acid

TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-92

CURRENT APPLICATION NUMBER: US/10/658,834A

CURRENT APPLICATION NUMBER: 06/457,135

PRIOR PILING DATE: 2003-09-09

PRIOR FILING DATE: 2003-09-09

PRIOR FILING DATE: 2002-09-09

NUMBER OF SEQ ID NOS: 1306

SOFTWARE: FESTSEQ for Windows Version 4.0
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APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Divertenti, Lila
APPLICANT: Divertenti, Lila
APPLICANT: Diverting Community
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nury
TITLE OF INVENTION: Molecules and Related Applications
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-92
CURRENT ELLING DATE: 2003-09-08
FRIOR PILLING DATE: 2003-09-08
PRIOR PILLING DATE: 2002-09-09
PRIOR FILLING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 897
TENGTH: 181
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Pred. No. 0.045;
2; Mismatches 6; Indels
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Best Local Similarity 57.9%;
Matches 11; Conservative
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Best Local Similarity 57.9
Matches 11; Conservative
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APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
            Vega, Manuel
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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US-10-658-834A-897
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Sequence 217, Application US/20040132977A1

GENERAL INFORMATION:
CENTERAL INFORMATION:
CENTERAL INFORMATION:
CHAPLICANT: Gayon, Thierry
APPLICANT: Gayon, Thierry
APPLICANT: Gayon, Thierry
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-92
CURRENT APPLICATION NUMBER: US/10/658,834A
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR FILING DATE: 2003-09-09
PRIOR FILING DATE: 2002-09-09
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Pred. No. 0.045;
2; Mismatches 6; Indels
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CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR PILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR PILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 198
LENGTH: 183
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank CAA00839
DATABASE ENTRY DATE: 1993-12-03
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DATABASE ENTRY DATE: 1993-06-28
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20040132977A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guy-on, Thierry
APPLICANT: Drittanti, Lila
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Best Local Similarity 57.9%;
Matches 11; Conservative
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Matches 11; Conserva
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US-10-658-834A-896
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US-10-658-834A-217
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APPLICANT: Garcier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Uside and Trier of Trier of Tuvery
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-922
CURRENT APPLICANTION NUMBER: US/10/658,834A
CURRENT PILING DATE: 2003-09-08
FRIOR APPLICATION NUMBER: 60/457,135
FRIOR APPLICATION NUMBER: 60/457,135
FRIOR PILING DATE: 2003-09-09
FRIOR APPLICATION NUMBER: 60/499,898
FRIOR PILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 901
LENGTH: 183
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APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.2%; Score 61; DB 16; Length 183; 57.9%; Pred. No. 0.045;
                                                                Molecules and Related Applications
    TITLE OF INVENTION: Acid

TITLE OF INVENTION: Molecules and Related Application Street 1922

FILE REFERENCE: 38751-922

CURRENT APPLICATION NUMBER: US/10/658,834A

CURRENT FILING DATE: 2003-09-08

PRIOR FILING DATE: 2003-03-21

PRIOR FILING DATE: 2002-09

PRIOR FILING DATE: 2002-09

PRIOR FILING DATE: 2002-09

PRIOR FILING DATE: 2002-09

SEQ ID NOS: 1366

SOFTWARE: FASEEQ for Windows Version 4.0

SEQ ID NO 900
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Best Local Similarity 57.9
Matches 11; Conservative
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Matches 11; Conservative
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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APPLICANT: Gantier, Lila
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Dittenti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: 108/10/658,834A
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR APPLICATION NUMBER: 60/467,135
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR PILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTMARE: FastSEQ for Windows Version 4.0
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Sequence 900, Application US/10658834A
Sequence 900, Application US/10658834A
Sequence 900, Application US/2040132977A1
SEQUENCE STATEMENT OF 
                       INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
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Pred. No. 0.045;
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Pred. No. 0.045;
TITLE OF INVENTION: Rational Evolution of Cytokines for High TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A
CURRENT PILING DATE: 2003-09-08
PRIOR PRIOR TILING DATE: 2003-09-09
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2002-09-09
PRIOR PRIOR FILING DATE: 2002-09-09
PRIOR PRIOR FILING DATE: 2002-09-09
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; Publication No. US20040132977A1
; GENERAL INFORMATION:
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Best Local Similarity 57.9'
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Best Local Similarity 57.9
Matches 11; Conservative
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US-10-658-834A-898
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; ORGANISM: Homo sapiens
US-10-658-834A-899
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RESULT 15
US-10-658-834A-903
; Sequence 903, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gartier, Rene
; APPLICANT: Gayo, Thierry
; APPLICANT: Gayo, Thierry
; TILLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TILLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TILLE OF INVENTION: Molecules and Related Applications
; TILLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 3875-922
; CURRENT FILING DATE: 2003-09-08
; PRIOR PLILING DATE: 2003-09-09
; PRIOR PLILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SEQ ID NO 903
; LENGTH: 183
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Molecules and Related Applications
             FILE REPERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A
CURRENT APPLICATION NUMBER: 60/457,135
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2003-09-09
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 902
LENGTH: 183
TYPE: PRI
TYPE: PRI
US-10-658-834A-902
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Best Local Similarity 57.9%;
Matches 11; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-903
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Search completed: March 30, 2005, 22:09:56 Job time : 16.1031 secs

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OM protein - protein search, using sw model

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US-10-828-343-2_COPY_87_105 103 1 GFNETSCLKKGLADGFFEFE 19 Title: Perfect score: Sequence:

BLOSUM62 Scoring table:

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Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

283416

length: 0 length: 2000000000 DB seq DB seq Minimum I Maximum I Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Length	DB	ΩI	Description
1	61	59.2	212	į	IVHUB2	interleukin-6 prec
7	55	53.4	208	~	T09216	
е	53	51.5	212	~	I46590	
4	23	51.5	212	N	146621	kin 6
S	51	49.5	207	~	I46084	interleukin 6 - ca
9	49	47.6	211	~	A34247	interleukin-6 prec
7	48.5	47.1	196	~	C95322	μ
ω	48	46.6	162	~	H83786	
đ	47	45.6	211	-	I CMS 6	ဖ
10	47	45.6	745	~	T05375	7
11	46	44.7	208	-	S29549	φ
12	46	44.7	568	~	C82379	response regulator
13	45	43.7	484	7	F71061	hypothetical prote
14	44	42.7	282	~	D70149	
15	44	42.7	454	~	T27249	
16	44	42.7	1893	~	T22661	
17	44	42.7	2875	Н	RRVUTW	н
18	44	42.7	4196	~	T43274	dynein heavy chain
19	43.5	42.2	233	~	AC2205	hypothetical prote
20	43	41.7	157	N	H69203	
21	43	41.7	208	Н	A56610	interleukin-6 prec
22	43	41.7	231	~	H83664	ribosomal protein
23	42.5	41.3	492	~	T30066	hypothetical prote
24	42	40.8	180	~	H72402	hypothetical prote
25	42	40.8	219	7	H88101	_
26	42	40.8	364	~	T23819	hypothetical prote
27	42		445	~	G98290	
28	42	40.8	445	7	AC2993	
29	42	40.8	512	0	847900	protein kinase RCK

primase - human he	microtubule bindin	genome polyprotein	vitellogenin - yel	genome polyprotein	genome polyprotein	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	vancomycin resista	hypothetical prote	hypothetical prote	gene cob intron 3	NMDA receptor-bind	glutathione transf
T41945	T13030	ZLNZSE	S46404	ZENZSV	ZLNZP3	E81443	T17748	E71208	S22615	JN0249	T51220	T00798	825952	T08880	JC2425
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ALIGNMENTS

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interleukin-6 precursor [validated] - human N;Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-cell

C;Species: Homo sapiens (man)
C;Species: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A35648; A25692; A2696; A33515; A25801; A25921; I52193; I55003; A27601; B27
R;Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishimot.
EMBO J. 6, 2939-2945, 1987
A;Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) gene
A;Reference number: A32648; MUID:88082664; PMID:3500852

A; Accession: A32648

A; Molecule type: DNA A; Residues: 1-212 < YAS>

A Cross-references: UNIPROT: P05231; GB: Y00081; NID: 929494; PIDN: CAA68278.1; PID: 929495 A; Note: the authors translated the codon CAG for residue 130 as Glu R;Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M. EMBO J. 5, 2529-2537, 1986 A; Title: Structure and expression of cDNA and genes for human interferon-beta-2, a distination of the companies of the

A; Accession: A25692

A; Molecule type: mRNA
A; Residues: 1-212 < ZIL>
A; Colection type: mRNA
A; Residues: 1-212 < ZIL>
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A; Molecule type: mRNA A; Residues: 1-212 <TON>

A;Cross-references: GB:M29150; NID:g186349; PIDN:AAA59154.1; PID:g307063
R;Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
Eur. J. Biochem. 159, 625-632, 1986
A;Title: Structural analysis of the sequence coding for an inducible 26-kDa protein in htalescence number: A25801; MUID:87004683; PMID:3758081

A;Cross-references: GB:X04403 A;Experimental source: fibroblast R;May, L.T.; Helfgott, D.C.; Sehgal, P.B.

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 28-40 cMAY3.
A; Rote: this 23-25K form contained O-linked but not N-linked carbohydrate
B; Oritia, T: Obeda, M:; Rasegawa, M.; Kuboniwa, H.; Esaki, K.; Ochi, N.
A; Note: this 23-25K form contained O-linked but not N-linked carbohydrate
B; Note: this 23-55K form carbohydrate structure of recombinant human interleukin-6 produc
A; File: Polypeptide and carbohydrate structure of recombinant human interleukin-6 produc
A; Contents: annotation; modified sites in recombinant protein from CHO cells
R; Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
A; Coltents: annotation; disulfide bonds in recombinant protein
B; R; Contents: annotation; disulfide bonds in recombinant protein
B; R; Contents: annotation; lability and functional significance of each disulfide bond
C; Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth factors lobulin secretion). It therefore appears to function as an autoregulator of cell growth c; C; Comment: This protein plays a regulatory role in various host defense mechanisms and er
C; Genetics:
A; Conserved C; Comment: This protein plays a regulatory role in various host defense mechanisms and er
C; Genetics: Areference complex complex complex complex complex conformation: A; Conserved complex comple
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A/Creie: UDD:121-7021

A/Introns: 7/1; 70/3; 108/3; 157/3

A/Introns: 7/1; 70/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/3; 108/
A;Note: sequence extracted from NCBI backbone
A;Note: this 28-30K form contained both N-linked and O-linked carbohydrate; a 25K form
A;Accession: C48419
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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R;Swiderski, C.E.; Horohov, D.W.
submitted to the EMBL Data Library, July 1996
A;Reference number: 216613
A;Accession: T09216
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C,Superfamily: interleukin-6
C,Keywords: cytokine; growth factor
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A; Residues: 1-208 <SWI>
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 29-42 < dHR2>
A; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; Az
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A; Title: Purification and characterization of human fibroblast derived differentiation i
A; Reference number: A61159; MUID: 91290785; PMID: 1648338
A; Molecule type: protein
A; Residues: 30-42 < NOD>

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A; Residues: 28-51, X',53-57, X',59, X',61 <VANL>
A; Residues: 28-51, X',53-57, X',59, X',61 <VANL>
A; Residues: 28-51, X',53-57, X',59, VX.;
A; Residues: 30-56, XXX,59-61, X',63 <VA2>
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A; Residues: 30-43 <AMN
A; Residues: 30-43 <AMN
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A; Reference number: A20085; MUID:8702370; PMID:3491991
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A) Residues: 1-212 (MON)
A) Cross-references: GB:M54894; NID:g186351; PIDN:AAC41704.1; PID:g186352
A) Cross-references: GB:M54894; NID:g186351; PIDN:AAC41704.1; PID:g186352
B; Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
J. Immunol. 139, 4116-4121, 1987
A) Title: Molecular cloning and expression of hybridoma growth factor in Escherichia coli A) Reference number: 156003; MUID:88088768; PMID:3320204
A) Accession: 156003
A) Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-212 <BRA>
A; Cross-references: GB:M18403; NID:g184631; PIDN:AAA52729.1; PID:g306911
A; Cross-references: GB:M18403; NID:g184631; PIDN:AAA52729.1; PID:g306911
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A; Title: Separation and comparison of two monokines with lymphocyte-activating factor ac
A; Reference number: A92816; MUID:88154445; PMID:3279116
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A;Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
A;Reference number: A25921; MUID:87067433; PMID:3538015
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R; May, L. T.; Shaw, J. E.; Khanna, A. K.; Zabriskie, J. B.; Sehgal, P. B.
Yctokine 3, 204-211, 1991
A;Title: Marked cell-type-specific differences in glycosylation of human interleukin-6.
A;Reference number: A48419; MUD:91355644; PMID:1883960
A;Accession: A48419
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A; Residues: 1-212 < KAXY>
A; Residues: 1-212 < KAXY>
A; Cross-references: GB:M14584; NID:g184628; PIDN:AAA52728.1; PID:g306910
R; Wong, G.G.; Witek-Giannotti, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
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A; Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
A; Reference number: I52193; MUID:89193317; PMID:3266463
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 30-37,'X',39-40 <MAY2>
A;Experimental source: FS-4 fibroblasts
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C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C;Accession: A4247
R;Northemann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
J. Biol. Chem. 264, 16072-16082, 1989
A;Title: Structure of the rat interleukin 6 gene and its expression in macrophage-derivec A;Reference number: A34247; MUID:89380206; PMID:2789217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRWA
A;Residues: 1-211 <NOR>-
A;Cross-references: UNIPROT:P20607; GB:M26744; NID:g204915; PIDN:AAA77659.1; PID:g204916
C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage
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C;Species: Sinorhizobium meliloti
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C;Accession: C95322
C;Accession: C95322
S;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse Froc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
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A;Residues: 1-196 <KUR>
A;Residues: 1-196 <KUR>
A;Residues: 1-196 <KUR>
A;Residues: 1-196 <KUR>
A;Residues: 1-196 <KUR>
A;Residues: 1-196 <KUR>
A;Ross-references strain 1021, megaplasmid pSymb
B;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.(A;Ttle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                               A;Residues: 1-207 <BRA>
A;Cross-references: UNIPROT:P41683; GB:L16914; NID:g438519; PIDN:AAA16620.1; PID:g438520
C;Superfamily: interleukin-6
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Pred. No. 2.2;
3; Mismatches
                                                                                                                                          Score 51; DB 2
Pred. No. 1;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                        101 GFNQETCLTRITTGLQEFQ 119
                                                                                                                                                                                                                                                        1 GFNETSCLKKLADGFFEFE 19
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                                                                                                                                          Query Match
Best Local Similarity 42.1%;
Matches 8; Conservative
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Best Local Similarity 44.4%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       interleukin-6 precursor - rat
        A; Molecule type: mRNA
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A;Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: P26893; GB: M86722; NID: 9164624; PIDN: AAC37333.1; PID: 9164625
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prointerleukin 6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: 146621
R;Richards, C:; Saklatva, J.
R;Richards, C:; Saklatva, J.
A;Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of A;Reference number: 146621; MUID:91338547; PMID:1873476
                                                                                                                                                                                                                                                                                                                                                                   and bovine preimplantation conce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
Proc. Soc. Exp. Biol. Med. 204, 301-305, 1993
A;Title: Molecular cloning and characterization of a cDNA encoding feline interleukin-6.
A;Reference number: 146084; MUID:94052249; PMID:8234373
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                                                                                                                                                                                      incerleukin 6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: 146590
R;Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A;Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplan
A;Reference number: 146590; MUID:92360284; PMID:1497880
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C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: 146084
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Bolcule type: mRNA
A,Residues: 1-212 <RIC>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 0.51;
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Pred. No. 0.51;
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                                                    102 GFNQETCLMKITTGLSEFQ 120
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GFNQETCLMRITTGLVEFQ 123
  GFNETSCLKKLADGFFEFE 19
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Best Local Similarity 42.1
Matches 8; Conservative
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A,Gene: IL-6
C,Superfamily: interleukin-6
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C,Superfamily: interleukin-6
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A; Residues: 1-212 < MAT>
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A,Modecule type: mRNA
A,Residues: 1-211 <CHI>
A,Cross-references: GB:J03783, NID:g198367; PIDN:AAA39301.1; PID:g309410
R;Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; Salood 72, 2070-2073, 1988
A,Fitle: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6.
A,Reference number: A60799; MUID:89062753; PMID:3264198
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F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-211/Product: interleukin-6 #status experimental <MAT>
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 25-166, 7%, 168-211 < SIM>
A; Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-As
B; Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
Nucleiac Acids Res: 18, 4655, 1990
Nucleiac Acids Res: 18, 4655, 1990
A; Fit.Le: Cloning and sequence analysis of the CDNA for murine interleukin-6.
A; Reference number: S12103; MUID:91057159; PMID:2243807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 66-69, X',71-75;78-94;128-148 <JA5>
R;Residues: 66-69, X',71-75;78-94;128-148 <JA5>
R;Van Snick, J.; Cayphas, S.; Vink, A.; Uyttenhove, C.; Coulie, P.G.; Rubira, M.R.; Simpt Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
A;Yitle: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine A;Reference number: A26662; MUID:87092311; PMID:2948184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Redidues: 25-39, X; 41-42, X', 44-45 <VSN>
R; Chiu, C.P.; Moulda, C.; Coffman, R.L.; Rennick, D.; Lee, F.
R; Chiu, C.P.; Moulda, C.; Coffman, R.L.; Rennick, D.; Lee, F.
A; Chiu, C.P.; Moulda, C.; Coffman, R.L.; Rennick, D.; Lee, F.
A; Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone
A; Reference number: A40486; MUID:89017145; PMID:3262872
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A;Residues: 77-98 <SHA>
X;Balmkenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A;Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a mon
A;Reference number: S10241; MUID:90171860; PMID:2106569
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Eur. J. Biochem. 217, 53-59, 1993
A;Title: Specific covalent modification of the tryptophan residues in murine interleukin-
A;Reference number: S38254; WUID:94039075; PMID:8223586
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728
R;Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
Biochem. Biophys. Res. Commun. 166, 139-145, 1990
A;Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage A;Reference number: A90157; MUID:90147691; PMID:2302197
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A;Molecule type: protein
A;Residues: 38-60;75,'X',77-79;176-203 <ZHA>
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A;Introns: 7/1; 68/3; 106/3; 156/3
C;Superfamily: interleukin-6
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Conservative
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nes 7; Conserv
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A; Residues: 1-211 <GRE>
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A;Molecule type: DNA
A;Residues: 1-6 <BLA>
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Best Local S
Matches 7
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H93786

H9374331, 2000

H71tle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132

H93786

H93886

H938
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C.Species: Mus musculus (house mouse)

C.Saccession: A30531; A27610; A30571; S01323; S12103; B34647; A26662; A40486; A60799; S10

R.Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.

J. Immunol. 141, 3875-3881, 1988

A;Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential A;Reference number: A30531; MUID:89035525; PMID:3263439
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A; Residues: 1-211 < vANA
A; Residues: 1-211 < vANA
A; Residues: 1-211 < vANA
A; Cross-references: GB: X06203; NID: 952701; PIDN: CAA29560.1; PID: 952702
R; Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Cla
A; Timmunol. 142, 1372-1376, 1989
A; Title: The murine 11-6 gene maps to the proximal region of chromosome 5.
A; Reference number: A30571; MUID: 99124383; PMID: 2563387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interleukin-6 precursor - mouse
N;Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M24221; NID:g341131; PIDN:AAA68814.1; PID:g870699
R;Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
Eur. J. Blochem. 176, 187-197, 1988
A;Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and A;Reference number: S01323; MUID:88329059; PMID:3262059
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                                                 Gaps
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Pred. No. 2.5;
                                            Indels
    Pred. No. 2.5;
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58.88;
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                                                                                                                                 2 FNETSCLKKLADGFFEF
Best Local Similarity 58.8
Matches 10; Conservative
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Best Local Similarity
--hem 10; Conserva
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A; Residues: 5-211 <MOC>
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C; Genetics:

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Gaps

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2; Length 568

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C;Accession: F71061
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekins M.; Offkuv, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic an A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: UNIPROT:058908; GB:AP000005; NID:g3236132; PIDN:BAA30288.1; PID:d103:A,Experimental source: strain OT3
A,Experimental source: strain OT3
A,Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PH1188 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
A;Gene: VCA1086
A;Map position: 2
C;Superfamily: response regulator, Hnr type; response regulator
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                                                                                                                                                       Score 46; DB 2
Pred. No. 18;
1; Mismatches
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177 YNNTSGSKKLEDSFF 191
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75 GYGKTSIMRALAEGIYDY
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                                                                                                                                                           Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: PH1188
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A;Experimental source: serogroup Ol; strain N16961; biotype El Tor
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C92379

response regulator VCA1086 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: C82379

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

R;Heidelberg, J.F.; Eisen, J.A.; Venter, J.C.; Praser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MuID:20406833; PMID:10952301
                                                                                                    hypothetical protein F16G20.70 - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress) Cispecies: Arabidopsis thaliana (mouse-ear cress) Cister 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 Cister Secession: T05375 Cister 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 4
A;Introns: 22/2; 121/1; 159/3; 234/3; 286/3; 366/3; 450/1; 490/3; 519/3; 572/3; 620/3
A;Note: F16G20.70
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#text_change 09-Jul-2004
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44.7%; Score 46; DB 1; Length 208;
Best Local Similarity 42.1%; Pred. No. 6.7;
Matches 8; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-745 <BEV>
A;Crose-references: UNIPROT:O81733; EMBL:AL031326
A;Experimental source: cultivar Columbia; BAC clone F16G20
C;Genetics:
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$29549
finterleukin-6 - sheep
Cypecies: Ovis orientalis aries, Ovis ammon aries
Cypecies: 10-Sep-1999 #sequence_revision 10-Sep-1999
CyAccession: S29549
R;Ebrahimi, B.
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A;Reference number: S29549
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-208 <EBR>
A;Cess-references: UNIPROT:P29455; EMBL:X68723
C;Superfamily: interleukin-6
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nes 8; Conserva
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A;Molecule type: DNA
A;Residues: 1-568 <HEI>
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                                 RESULT 10
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A;Experimental source: strain B31
Pypothetical protein BB0397 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: D: Poloty
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Non, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, R. Nature 390, 580-586, 1997
A;Tutle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-282 <KLE>
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hypothetical protein Y5F2A.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27249
R;Lennard, N.
submitted to the EMBL Data Library, October 1998
A;Recence number: 220331
A;Accession: T27249
A;Accession: T27249
A;Accession: T27249
A;Residues: 1-454 <MIL>
A;Residues: 1-454 <MIL>
A;Residues: 1-454 <MIL>
A;Residues: 1-544 <MIL>
A;Coss-references: UNIPROT:Q9XWLO; EMBL:AL032641; PIDN:CAA21647.1; GSPDB:GN00022; CESP:A;Experimental source: clone Y5F2A
C;Genetics:
C;Genetics:
A;Gene: CESP:Y5F2A.4
A;Map position: 4
A;Map position: 4
A;Introns: 17/2; 50/3; 125/3; 159/3; 201/3; 241/2; 353/1; 411/1
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42.7%; Score 44; DB 2; Length 454;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 10; Conservative 2; Mismatches 2; Indels
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Job time : 5.5157 secs
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177 HETSCLKKFAFVCKPCDSYF 196
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gallus gall
equus cabal
phoca vitul
canis famil
canis famil
sus scrofa
sus scrofa
lama glama
camelus bac
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aotus nigri
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MEDLINES-97296220; PubMed=9151804;
MEDLINES-97296220; PubMed=9151804;
Neipel F., Albrecht J.C., Fleckenstein B.;
"Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
"Muman herpesvirus 8: determinants of its pathogenicity?";
J. Virol. 71:4187-4192(1997).
                                                                                                                                                                                                                                                                                          Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
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MEDLINE=97138401; PubMed=8985427;
Neipel R., Albrecht J.C., Ensser A., Huang Y.Q., Li J.J.,
Friedman-Kien A.E., Fleckenstein B.;
"Human herpesvirus 8 encodes a homolog of interleukin-6.";
J. Virol. 71:839-842(1997).
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PRINTS; PRO0434; INTERLEUKING.
PROD00m; PD004356; Interleukin_6; 1.
SMART; SMO0126; IL6; 1.
SEQUENCE 204 AA; 23407 MW; 2P467378200D20B9 CRC64;
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Pred. No. 4.7e-08;
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InterPro; IPR003573; II6 MGF GCSF.
InterPro; IPR001574; Interleukin_6.
Pfam; PF00489; IL6; 1.
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NCBI_TaxID=37296;
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"A single 13-kilobase divergent locus in the Kaposi sarcoma-associated herpesvirus (human herpesvirus 8) genome contains nine open reading frames that are honologous to or related to cellular proteins.";
J. Virol. 71:1963-1974(1997).
                                                                                                                                                                                                             Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
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Viruses; dBODA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
VGBI_TaxID=37296;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
0RF K2; functional interlenkin-6 vIL-6 homolog (Putative interleukin
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Nicholas J., Ruvolo V.R., Burns W.H., Sandford G., Wan X., Ciufo D.,
Hendrickson S.B., Guo H.G., Hayward G.S., Reitz M.S.;
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MEDLINE=97184526; PubMed=9032328;
Nicholas J., Ruvolo V., Zong J., Ciufo D., Guo H.G., Reitz M.S.,
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GO; GO:0005125; F:cytokine activity, IEA.
GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
GO; GO:00069579; F:immune response; IEA.
InterPro; IPRO09079; 4 helix_cytokine.
InterPro; IPRO09079; 4 helix_cytokine.
InterPro; IPRO09079; Infe MGF GCSF.
InterPro; IPRO049574; Interleukin_6.
Pfam; PRO0499; IL6; 1.
PRINTS; PRO0413; ILGCSCRMGF.
PRINTS; PRO0414; INTERLEUKING.
PRODOM; PO0456; Interleukin_6; 1.
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EMBL; U73655; AAB18244.1; -.
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                                                                                                                                                                                                                                                                           NCBI_TaxID=37296;
                                                                                                   01-FEB-1997
                                                                                                                                                                                         Name=vIL-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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               RESULT 2
Q98823
ID Q98823
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7065K3
TO 7065K3
AC 0765K3
DT 05-JI
DT 05-JI
DT 05-JI
DE 00K 1
DE 00 VITUM
CO VITUM
CO COMMENT
RAM HAYW
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Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D., Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

Bubl. (05774; AA661701.1; -...

EMBL; U71365; AAC34937.1; -...

REMBL; U71365; AAC37089.1; -...

ROJ, GO:000576; C:extracellular; IEA.

GO; GO:0005138; F:interleukin-6 receptor binding; IEA.

ROJ; GO:0006955; P:immune response; IEA.

ROJ; GO:0006955; P:immune response; IEA.

ROJ; GO:0006955; P:immune response; IEA.

RITEPPO; IPR00979; 4 helix_cytokine.

RITEPPO; IPR003574; Interleukin-6.

RITEPPO; IPR003574; Interleukin-6.
"Kaposi's sarcoma-associated human herpesvirus-8 encodes homologues of macrophage inflammatory protein-1 and interleukin-6."; Nat. Med. 3:287-292(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEGUENCE FROM N.A.
MEDLINE=97121480; PubMed=8962146; DOI=10.1073/pnas.93.25.14862;
MEDLINE=97121480; PubMed=8962146; DOI=10.1073/pnas.93.25.14862;
MENSO J.J., Bohenzky K.A., Chien M.-C., Chen J., Yan M., Maddalena D., Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
"Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE=22354194; PubMed=12466897; DOI=10.1007/800251-002-0512-2;
Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
Murillo L.A., Patarroyo M.E.;
Identification, cloning, and sequencing of different cytokine genes
in four species of owl monkey.";
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=97094384; PubMed=8939871; DOI=10.1126/science.274.5293.1739;
Moore P.S., Boshoff C., Welss R.A., Chang Y.;
"Molecular mimicry of human cytokine and cytokine response pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Platyrrhini, Cebidae, Aotinae, Aotus.
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                                                                                                                                          SEQUENCE FROM N.A.
Sun R., Lin S.-F., Miller G.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 AA; 23408 MW; 1CA7772A0EDC05EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
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Last sequence update)
Last annotation update)
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PRINTS; PRO0434; INTERLECKING.
PPODOM; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                        genes by KSHV.";
Science 274:1739-1744(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-6 (Fragment).
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105 GFNEETCLLKITTGLLEFE 123
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                                                                     RESULT 6
Q8MKH0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aotus nigriceps (Black-headed owl monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22354194; PubMed=12466897; DOI=10.1007/800251-002-0512-2; Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J., Murillo L.A., Patarroyo M.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   60.2%; Score 62; DB 2; Length 175; 57.9%; Pred. No. 0.12; tive 2; Mismatches 6; Indels
                EMBL; AF014505; AAD01531.1; -...
HSSP; P05231; 1IL6.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytckine activity; IEA.
GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
GO; GO:000555; P:immune response; IEA.
InterPro; IPR009079; 4 helix cytckine.
InterPro; IPR000573; IL6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 160 AA; 17855 MW; 07A021338650A46D CRC64;
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GO; GO:0005125; F:cytckine activity; IEA.
GO; GO:0005138; F:nterleukin-6 receptor binding; IEA.
GO; GO:000555; P:immune response; IEA.
InterPro; IPR009079; 4 helix cytckine.
InterPro; IPR003573; IL6 MGP GCSF.
InterPro; IPR003573; Interleukin-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                   PEAM, PRO0489, IL6; 1.
PRINTS; PRO0433; ILGGCSFNGF.
PRINTS; PRO0434; INTERLEUKIN6.
SPROOMS; PRO0436; Interleukin 6; 1.
SMART; SMO0126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS, PRO0433, ILGGCSFWGF.
PRINTS, PRO0434; INTERLEUKING.
PRO00m; PD004356; Interleukin_6; 1.
SWART; SM00126; ILG; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
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Immunogenetics 54:645-653(2002).
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Best Local Similarity
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Best Local Similarity
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4.0 TTH

4.0 OFTH

7.0 OFTH

DT 01-M

DT 01-M

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OC 09TTH

OC 09TH

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1 GFNETSCLKKLADGFFEFE 19

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Saimiri sciureus (Common squirrel monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
NCBI_TaxID=9521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=21972723; PubMed=11976788; DOI=10.1007/800251-002-0443-y; Heraud J.M., Lavergne A., Kazanji M.; M.; "Molecular cloning, characterization, and quantification of squirrel monkey ( Saimiri sciureus) Thl and Th2 cytokines."; Immunogenetics 54:20-29(2002).

EMBL; AF294757; AAK92044.1; -.

HSSP; P05231; 116.
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Mammalia; Eutheria, Primates, Platyrrhini, Cebidae, Aotinae, Aotus.
NCBI_TaxID=37293;
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GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005138; F:chterleukin-6 receptor binding; IEA.
GO; GO:000555; P:immune response; IEA.
InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR003573; IL6 MGF GGSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PP00489; IL6; 1.
                                 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.2%; Score 62; DB 2;
57.9%; Pred. No. 0.14;
tive 2; Mismatches
  212 AA
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GO; GO:0005125; F:cytokine activity; IEA.
PRT;
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PRINTS; PR00434; INTERLEUKING.
PRODOM; PD004356; Interleukin_6; 1.
SWART; SW00126; ILG; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
SEQUENCE 212 AA; 23581 MW; FP22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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les 11; Conservative
PRELIMINARY;
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01-NOV-1995
01-NOV-1995
                                         IL6 CERTO
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SEQUENCE
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Matches
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IL6_HUMAN
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MEDLINE=22354194; PubMed=12466897; DOI=10.1007/800251-002-0512-2;
Hernandez E.C., Suarez C.P., Mendez J.A., Echeverry S.J.,
Muxillo L.A., Pararcoyo M.E.;
"Identification, cloning, and sequencing of different cytokine genes
in four species of owl monkey.";
Immunogenetics 54:645-653(2002).
EMBL; AP097323; AAF21298.1; -.
HSSP; P05231; IALU.
                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aotus lemurinus (Northern gray-necked night monkey).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBI_TaxID=43147;
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Pred. No. 0.2;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                  Score 61; DB 2; Length 209;
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                           209 AA; 23406 MW; E84F085DD84002DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 209
209 AA; 23115 MW; AOA3DFAA4BF560CC CRC64;
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GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR003573; IL6 MGF GCSF.
InterPro; IPR003574; Interleükin_6.
Pfam; PP00489; IL6; 1.
GO:0005138; F:interleukin-6 receptor binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 AA
                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                    GO; GO:0006955; P:immune response; IEA InterPro; IPR0036079; 4 helix cytokine. InterPro; IPR003573; II6 MGF GCSF. InterPro; IPR003574; Interleukin_6.
                                                                                           PEGN; PRO0489; ILG; 1.
PRINTS; PR00433; ILGGCSFWGF.
PRINTS; PR00434; INTERLEUKING.
PRODOM; PD004356; Interleukin_6; 1.
SWART; SW00126; ILG; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
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PRINTS; PR00434; INTERLEUKING.
ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
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108 11; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nonhuman primates.,;
J. Immunol. 155:13946-3954(1995).

-!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
-!- FUNCTION: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and
plasmacytoma growth, it induces nerve cells differentiation, in
hepatocytes it induces acute phase reactants.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                             Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey) Bukaryota, Metacoa; Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates; Catarrhini; Cercopithecidae; Cercopithecidae; Cercopithecidae; Cercopithecidae; Cercopithecidae; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=FUJ;
MEDLINE=96003435; PubMed=7561102;
Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
"Comparative sequence analysis of cytokine genes from human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
SIGNAL
1 29 By similarity.
CHAIN
2 By similarity.
DISULFID 72 78 By similarity.
DISULFID 101 111 By similarity.
CARBOHYD 172 172 N-linked (GloNAC. .) (Potential)
CARBOHYD 172 172 N-linked (GloNAC. .) (Potential)
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                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Interpro; IPR003573; II6 MGF GCSF.
Interpro; IPR003574; Interleukin_6.
Pfam; PF00489; II6; 1.
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PRINTS; PRO0434; INTERLEUKING.
POCODON; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
   PRT;
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105 GFNEDTCLVKIITGLLEPE 123
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                                                                                                                                                                              Interleukin-6 precursor (IL-6)
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HSSP; P05231; 1ALU.
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9531;
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=87065033; Pubmed=3491322;
Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,
Kashiwamura S.-I., Makajima K., Koyama K., Iwamatsu A., Tsunasawa S.,
Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
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B lymphocytes to produce immunoglobulin.";
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"Structure and expression of cDNA and genes for human interferon-beta-
2, a distinct species inducible by growth-stimulatory cytokines.";
EMBO J. 5:2529-2537(1986).
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"Anti-beta-interferon antibodies inhibit the increased expression of
HLA-B7 mRNA in termor necrosis factor-treated human fibroblasts:
structural studies of the beta 2 interferon involved.";
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25-OCT-2004 (Rel. 45, Last annotation update)
Interleukin-6 precursor (IL-6) (B-cell stimulatory factor 2) (BSF-2)
(Interferon beta-2) (Hybridoma growth factor) (CTL differentiation
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Nakai S., Kishimoto T.;
"Structure and expression of human B cell stimulatory factor-2 (BSF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wong G., Witek-Giannotti J., Hewick R., Clark S., Ogawa M.;
"Interleukin 6: identification as a hematopoietic colony-stimulating
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Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
"Deletion of 3' untranslated region of human BSF-2 mRNA causes
stabilization of the mRNA and high-level expression in mouse NIH3T3
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                                                                                                                                                                                          ronno apptens, fundant.
Bukaryota, Metazoa, fordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88088768; PubMed-3320204;
Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
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Eur. J. Biochem. 159:625-632(1986).
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MEDLINE=88082664; Pubmed=3500852;
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J. Immunol. 139:4116-4121(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBO J. 6:2939-2945(1987).
                                                                                                                                         Name=IL6; Synonyms=IFNB2;
Homo sapiens (Human).
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                                                                                                         (CDF).
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   ERREAR SEED OOG SOOR SEED OF S
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factor.";
Behring Inst. Mitt. 83:40-47(1988)

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TISSUB-LUNG;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12479932; DOI=10.1073/pnas.2426099;

MEDLINE=2238269; MEDLINE=247999;

MEDLINE=2238269; MEDLINE=247999;

MEDLINE=2238269; MEDLINE=247999;

MEDLINE=2238269;

MEDLINE=238269;

MEDLINE=2238269;

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MEDLINE=90121567; PubMed=2610854;

Ming J.E., Cernetti C., Steinman R.M., Granelli-Piperno A.;

Ming J.E., Cernetti C., Steinman R.M., Granelli-Piperno A.;

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J. Mol. Cell. Immunol. 4:203-211(1989).
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MEDLINE-9135644; DubMed=188366; DOC=10.1016/1043-4666(91)90018-9;
MARY L.T., Shaw J.E., Khannan A.K., Zabriskie J.B., Sehgal P.B.;
"Marked cell-type-specific differences in glycosylation of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 30-63.
MEDLINE-88154445; PubMed=3279116;
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Billiau A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Nickerson D.A.;
"SeattleSNBs. NHLBI HL6682 program for genomic applications,
"ReattleSNBs. NHLBI (HL6682), // pga.gs washington.edu).";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           ROM N.A., AND VARIANTS SER-32 AND VAL-162.
., Carrington D.P., Chung M.-W., Lee K.L., Poel
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                               SEQUENCE FROM N.A.
MEDLINE=93178270; PubMed=1291290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB000554; BAA19148.1; -. HSSP; P05231; 11L6.
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PRINTS; PR00434; INTERLEUKING.
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57.9%;
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nes 11; Conservative
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NCBI_TaxID=9544;
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73
172
212 AA;
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        NCBI_TaxID=9541;
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IL6 MACMU
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MEDLINE=97224126; PubMed=9118960; DOI=10.1093/emboj/16.5.989;

MEDLINE=97224126; PubMed=9118960; DOI=10.1093/emboj/16.5.989;

MEDLINE=97224126; PubMed=9118960; DOI=10.1093/emboj/16.5.989;

MEDLINE=97224126; PubMed=9118960; DOI=10.1093/emboj/16.5.989;

MEDLINE=97224126; PubMed=30.18.3.;

MEDLINE=9724126; PubMed=30.18.3.;

MEDLINE=99; POINTION: The first implications for a novel and effections: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants.

MEDLINESELULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: Secreted.

SUBCE
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                                                                                                                                    MUTAGENESIS.
MEDLINE=91243808; PubMed=2037043; DOI=10.1016/0014-5793(91)80491-K;
MEDLINE=91243808 A., Moeller C., Heinrich P.C., Rose-John S.;
Luetticken C., Kruettgen A., Moeller C., Heinrich P.C., Rose-John S.;
Evidence for the importance of a positive charge and an alpha-helical
structure of the C-terminus for biological activity of human IL-6.";
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96134845; PubMed=8555185; DOI=10.1021/bi951949e;
Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
"Folding topologies of human interleukin-6 and its mutants as studied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.; "Disulfide structures of human interlaukin-6 are similar to those of human granulocyte colony stimulating factor."; Arch. Biochem. Biophys. 272:144-151(1989).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97303053; PubMed=9159484; DOI=10.1006/jmbi.1997.0933; Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E., Cumming D.A.; Stahl M., McDonagh T., Kay L.E., E., Cumming D.A.; Statictore of recombinant human interleukin-6."; J. Mol. Biol. 268:468-481(1997).
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Pred. No. 0.21;
2; Mismatches 6; Indels
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-6 precursor (IL-6).
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                                                                                                                                                                                                                                                                          Lett. 282:265-267(1991).
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1 Similarity 57.9%;
11; Conservative
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15-JUL-1998
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                                                                                                                            -I-FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into IG-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-6 superfamily.
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Tatsumi M.;
"Molecular cloning and expression of cynomolgus monkey interleukin-
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
"Comparative sequence analysis of cytokine genes from human and
nonhuman primates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.

By similarity.
N-linked (GloNac. .) (Potential)
N-linked (GloNac. ..) (Potential)
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                                                                                                  Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Pred. No.
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Interpro; IPR003573; II6 MGF_GCSF.
Interpro; IPR003574; Interleukin_6.
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PMCSTTE; SMOLZ56; ILG.; 1.

RCSTTE; PS00254; INTERLUXIN 6; 1.

Acute phase; Cytokine; Glycoprotein; CSTGNAL 30 212 By similar 10 111 By similar 10 111 By similar 10 111 By similar 10 111 By similar 173 73 N-linked CARBOHYD 172 172 N-linked
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    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Matches
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                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in heparocytes it induces acute phase reactants (By similarity). SubCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wigley P.; ""Limeral L., Galyov E.E., Barrow P.A., Burnside J., "Differential cytokine expression in avian cells in response to invasion by Salmonella typhimurium, Salmonella enteritidis and Microbiology 146:3217-3226(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     By similarity.

By similarity.

N-linked (GlCNAc. ..) (Potential)

N-linked (GlCNAc. ..) (Potential)
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Kaiser P., Rothwell L., Galyov E.E., Barrow P.A., Burnside J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 61; DB 1; Length 212;
Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaspers B., Staeheli P.;
the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4130DFE0CF0BCCAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                      SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By similarity,
Interleukin-6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR003573; IL6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0433; ILGGCSFMGF.
PRINTS; PRO0434; INTERLEUKING.
PRODOM; PD004356; INTERLEUKING;
SMART; SM00126; ILG; 1.
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155:3946-3954 (1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23728 MW;
                                                                                                                                                                                                                                                                                                                                    EMBL; L26028; AAA99978.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Submitted (FEB-2001) to
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Gallus gallus (Chicken)
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78
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73
172
172 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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"Cloning and expression of equine interleukin-6.";

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into 1g-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).

-!- SUBCELLUIAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the IL-6 superfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.3%; Score 58; DB 2; Length 241; 52.6%; Pred. No. 0.7; 6; Indels ive 3; Mismatches 6; Indels
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ309540; CAC40812.1; -.
EMBL; AJ508939; CAC15566.2; -.
HSSP; P05231; IALU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 mature ChIL-6.
26790 MW; 657F8049F25BD2F8 CRC64;
                                                                                                                                            GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
GO; GO:000695; P:immune response; IEA.
PEAM; PRO0439; ILG; 1.
PRINTS; PRO0433; ILGGCSFMGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGHORSE STANDARD; PRT; 208 AA. 095181; 019007; 046568; 01-NOV-1997 (Rel. 35, Created) 15-UL-1999 (Rel. 38, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vet. Immunol. Immunopathol. 77:213-220(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                         Prodom; PD008388; GCSF_MGF; 1.
Prodom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||:| || ||: | ||:
126 GFDEEKCLTKLSSGLFAFO 144
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es 10; Conservative
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Matches
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A King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
A Stott J.L., Ferritch D.A.;
Indecular cloning and sequencing of interleukin 6 cDNA fragments from
the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
southern sea oteer (Enhydra lutris nereis).";
Immunogenetics 43:190-195(1996).
Immunogenetics 43:190-195(1996).
Immunogenetics 43:190-195(1996).
C --- FUNCTION: It plays an essential role in the final differentiation
of Bacchis into Ig-secreting cells, it induces myeloma and
plasmacytem growth, it induces nerve cells differentiation, in
hepatcoytes it induces acute phase reactants (By similarity).
C --- SUBCELLULAR LOCATION: Secreted.
C --- SIMILARITY: Belongs to the IL-6 superfamily.
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 Interleukin-6.
75 By similarity.
108 By similarity.
71 N-linked (GlCNAc. .) (Potential).
184 N-linked (GlCNAc. .) (Potential).
5 LS -> FF (in Ref. 1).
8 T -> A (in Ref. 2).
137 I -> V (in Ref. 2).
205 V -> I (in Ref. 2).
A, 23325 MW, A62P4C234056BF66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phoca vitulina (Harbor seal).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Pinnipedia, Phocidae, Phoca.
                                                                                                                                                                                                                                                                                                 InterPro; IPRUC.

InterPro; IPRUC.

A Fam; PP00489; IL6; 1.

DR PRINTS; PR00449; IL6; 1.

DR PRINTS; PR00449; INTERLEUKING.

DR PRINTS; PR00449; INTERLEUKING.

DR SWART; SW00126; IL6; 1.

DR SWART; SW00126; IL6; 1.

DR ROSITE; PS00254; INTERLEUKING.

DR SWART; SW00126; IL6; 1.

DR SWART; SW00126; IL6; 1.

DR SWART; SW00126; IL6; 1.

TO POCENTIAL

FT CHAIN

TO SULFID 98 108 By similarity.

TO TO N-linked (GlCNAC. ...) (Potent.

TO TO N-linked (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
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30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-6 precursor (IL-6) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 AA
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                                                                                                                                     EMBL; U64794; AAB87703.1; -.
EMBL; AF005227; AAB62246.1; -.
EMBL; AF09195; AAC04574.1; -.
PIR; T09216; T09216.
HSSP; P05231; 1ALU.
InterPro; IPR003979; 4 helix_cytokine.
InterPro; IPR003573; IL6 MSF GCSF.
InterPro; IPR003574; Interleukin_6.
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Q28819;
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116 PHOVI
110 116 PHOVI
10 028 B1
10 116 PHOVI
130 -MA
DT 30 -MA
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